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=> fil hcaplus
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FILE COVERS 1907 - 13 Feb 2003  VOL 138 ISS 7
FILE LAST UPDATED: 12 Feb 2003  (20030212/ED)

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.


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=> d stat que l7
L1             1 SEA FILE=REGISTRY ABB=ON  PLU=ON  WVRWHF/SQSP
L2            38 SEA FILE=REGISTRY ABB=ON  PLU=ON  W{GAILVSTR}[GAILVSTR]WHF/SQSP

L3             1 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L1
L4            27 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L2
L5             1 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L3 AND L4


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=>

=> d ibib abs hitrn l7 1

L7   ANSWER 1 OF 1  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         2000:535163  HCAPLUS
DOCUMENT NUMBER:          133:143915
TITLE:                    Transcription factor E2F DNA-binding domain inhibitor
                          peptides and uses thereof
INVENTOR(S):              Muller, Rolf; Kontermann, Roland Ernst; Montigiani,
                          Silvia
PATENT ASSIGNEE(S):       Prolifix Limited, UK
SOURCE:                   PCT Int. Appl., 42 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

      PATENT NO.          KIND  DATE          APPLICATION NO.  DATE
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      WO 2000042212       A1    20000720      WO 2000-GB98     20000113
          W:  AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU,
              CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL,
              IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA,
              MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI,
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SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM,
AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE,
DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF,
CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
CA 2359143 AA 2 [illegible] CA [illegible]
EP 1144443 A1 2 [illegible] EP [illegible]
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, NL, SE, MC, PT,
IE, SI, LT, LV, FI, RO
US 20030130309 A1 [illegible] US [illegible]
PRIORITY APPLN. INFO.: GB 1999-1710 A 19990126
WO 2000-GB227 W 20000126

OTHER SOURCE(S): MARPAT 133:145915

AB The present invention provides sequences of peptides which bind to the DNA binding domain of transcription factor E2F, and inhibit cell cycle progression. Peptides include FWLRFT, WYRWHF, WHFIFW, IWLSGLSRGVWWSFP, and GSRILTFRSGSWYAS and derivs. based upon these sequences. Compns. and the use of the peptides in inhibiting cell cycle progression, such as in uncontrolled cell proliferation, are also provided.

IT **286839-16-5P**
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); SPN (Synthetic preparation); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(peptide sequence; transcription factor E2F DNA-binding domain inhibitor peptides and uses thereof)

IT **286839-22-3 286839-23-4**
RL: PRP (Properties)
(unclaimed sequence; transcription factor E2F DNA-binding domain inhibitor peptides and uses thereof)

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

=> select hit rn 1T 1
E1 THROUGH E1 ASSIGNED

=> fil reg
FILE 'REGISTRY' ENTERED AT 13:50:51 ON 13 FEB 2003
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STRUCTURE FILE UPDATES: 11 FEB 2003 HIGHEST RN 469395-63-1
DICTIONARY FILE UPDATES: 12 FEB 2003 HIGHEST RN 469395-63-1

TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002

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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP PROPERTIES for more information. See STNote 27, Searching Properties in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES stnotes27.pdf

[illegible]
1 [illegible] B1

[286839-16-5/BN]
1 286839-22-3/BI
[286839-22-3/BN]
1 286839-23-4/BI
[286839-23-4/BN]
L8 3 [286839-16-5/BI OR 286839-22-3/BI OR 286839-23-4/BI] AND (L1 OR L2 OR L3)

=> d .seq l8 1-3

L8 ANSWER 1 OF 3 REGISTRY COPYRIGHT 2003 ACS
RN **286839-23-4** REGISTRY
CN L-Phenylalanine, L-tryptophyl-L-alanyl-L-arginyl-L-tryptophyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 13: PN: WO0044771 SEQID: 22 unclaimed sequence
SQL 6
RN **286839-23-4** REGISTRY

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HITS AT: 1-6

REFERENCE 1: 133:145915

L8 ANSWER 2 OF 3 REGISTRY COPYRIGHT 2003 ACS
RN **286839-22-3** REGISTRY
CN L-Phenylalanine, L-tryptophyl-L-alanyl-L-arginyl-L-tryptophyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 12: PN: WO0044771 SEQID: 21 unclaimed sequence
SQL 6
RN **286839-22-3** REGISTRY

SEQ 1 WARWHF
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HITS AT: 1-6

REFERENCE 1: 133:145915

L8 ANSWER 3 OF 3 REGISTRY COPYRIGHT 2003 ACS
RN **286839-16-5** REGISTRY
CN L-Phenylalanine, L-tryptophyl-L-valyl-L-arginyl-L-tryptophyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2: PN: WO0044771 SEQID: 2 claimed sequence
SQL 6
RN **286839-16-5** REGISTRY

SEQ 1 WVRWHF
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HITS AT: 1-6

REFERENCE 1: 133:145915

=> d stat que l11

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L5 1 SEA FILE=HCAPLUS ABB=ON PLU=ON [illegible]

L6 [illegible] SEA FILE=HCAPLUS ABB=ON PLU=ON [illegible]

L7 1 SEA FILE=HCAPLUS ABB=ON PLU=ON [illegible] AND [illegible]

L11 26 SEA FILE=HCAPLUS ABB=ON PLU=ON L6 NOT L7

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=> d ibib abs hitrn l11 1-26

L11 ANSWER 1 OF 26 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:850304 HCAPLUS

DOCUMENT NUMBER: 137:347570

TITLE: Cloning and cDNA and deduced amino acid sequences of 69 human proteins and their diagnostic and therapeutic uses

INVENTOR(S): Ruben, Steven M.; [illegible]; [illegible]; Birse, Charles E.

PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA

SOURCE: U.S. Pat. Appl. Publ., 194 pp., Cont.-in-part of Appl. No. PCT/US01/01346. CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 90

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002165137	A1	20021107	US 2001-860670	20010521
WO 2001055449	A1	20010802	WO 2001-US1346	20010117

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
AU 2001050770	A5	20010807	AU 2001-50770	20010117
US 2002042096	A1	20020411	US 2001-764[illegible]	[illegible]
US 20020772[illegible]	A1	[illegible]	US 2001-7648[illegible]	[illegible]
US 20020868[illegible]	A1	[illegible]	US 2001-7648[illegible]	[illegible]
US 2002086820	A1	20020704	US 2001-76486[illegible]	20010117
US 2002086821	A1	20020704	US 2001-764881	20010117
US 2002086822	A1	20020704	US 2001-764886	20010117
US 2002086823	A1	20020704	US 2001-764889	20010117
US 20020868[illegible]	A1	20020704	US 2001-764893	20010117
US 2002090615	A1	20020711	US 2001-76487[illegible]	20010117
US 2002090674	A1	20020711	US 2001-7649[illegible]	20010117
US [illegible]	A1	200207[illegible]	US 2001-7648[illegible]	20010117
US [illegible]	A1	200208[illegible]	US 2001-764846	20010117
US 20021199[illegible]	A1	200208[illegible]	US 2001-764855	20010117
US 20021[illegible]	A1	200209[illegible]	US 2001-76484[illegible]	20010117
US 2002014[illegible]	A1	[illegible]	US 2001-7648[illegible]	[illegible]

US 2002151479	A1	[illegible]	US 2001-764[illegible]		[illegible]
US 200216125[illegible]	A1	[illegible]	US 2001-764[illegible]		[illegible]
US 2002164[illegible]	A1	[illegible]	US 2001-764857		20010117
US 2002173454	A1	20021121	US 2001-764904		20010117
US 2003013649	A1	20030116	US 2001-989442		20011121
PRIORITY APPLN. INFO.:			US 2000-179065P	P	20000131
			US 2000-179065P	P	20000131
			US 2000-180628P	P	20000204
			US 2000-180628P	P	20000204
			US 2000-21[illegible]P	P	[illegible]
			US 2000-216[illegible]P	P	[illegible]
			US 2000-21[illegible]P	P	20000714
			US 2000-22[illegible]P	P	[illegible]
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			[illegible]	P	[illegible]
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			US 2000-249210P	P	20001117
			US 2000-249211P	P	20001117
			US 2000-249214P	P	20001117
			US 2000-249265P	P	20001117
			US 2000-250160P	P	20001201
			US 2000-250391P	P	20001201
			US 2000-251030P	P	20001205
			US 2000-251988P	P	20001205
			US 2000-256719P	P	20001205
			US 2000-251479P	P	[illegible]
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			[illegible]	P	[illegible]
			[illegible]	P	[illegible]
			US 2001-764[illegible]	A2	[illegible]
			WO 2001-US1346	A2	20010117
			US 2000-214886P	P	20000628
			US 2000-216647P	P	20000707
			US 2000-217487P	P	20000711
			US 2000-217496P	P	20000711
			US 2000-22[illegible]963P	P	[illegible]
			US 2000-22[illegible]964P	P	20000726
			US 2000-22451[illegible]P	P	20000814
			US 2000-224519P	P	20000814
			US 2000-225267P	P	20000814
			US 2000-225268P	P	20000814
			US 2000-225270P	P	20000814
			US 2000-225757P	P	20000814
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US	2000-236327P	P	20000929
US	2000-236368P	P	20000929
US	2000-236369P	P	20000929
US	[illegible]	[illegible]	[illegible]
US	[illegible]	[illegible]	[illegible]
US	[illegible]	[illegible]	[illegible]
US	[illegible]	[illegible]	[illegible]
US	2000-239040P	P	20001002
US	2000-241785P	P	20001020
US	2000-241809P	P	20001020
US	2000-244617P	P	20001101
US	2000-249299P	P	20001117
US	2000-251356P	P	20001208
US	2000-251868P	P	20001208
US	2000-251869P	P	20001208
US	2001-764863	B1	20010117

AB The present invention relates to 69 novel human proteins and isolated nucleic acids contg. the coding regions of the genes encoding such proteins. Tissue distribution, sequence homologies, and preferred epitope sites are provided for the proteins, as well as chromosomal mapping of some of the genes. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human proteins in bacterial, insect, and mammalian cells. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human proteins. High-throughput screening assays are also provided for various putative activities of the proteins.

IT **474183-38-5P**, Protein (human clone HFIEC13)
RL: BPN (Biosynthetic preparation ; BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; cloning and cDNA and deduced amino acid sequences of 69 human proteins and their diagnostic and therapeutic uses)

L11 ANSWER 2 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:723049 HCAPLUS
DOCUMENT NUMBER: 137:227411
TITLE: Whole-genome comparison of Mycobacterium tuberculosis clinical and laboratory strains
AUTHOR(S): Fleischmann, R. D.; Alland, D.; Eisen, J. A.; Carpenter, L.; White, O.; Peterson, J.; DeBoy, R.; Dodson, R.; Gwinn, M.; Haft, D.; Hickey, E.; Kolonay, J. F.; Nelson, W. C.; Umayam, L. A.; Ermolaeva, M.; Salzberg, S. L.; Delcher, A.; Utterback, T.; Weidman, J.; Khouri, H.; Gill, J.; Mikula, A.; Bishai, W.; Jacobs, W. R., Jr.; Venter, J. C.; Fraser, C. M.
CORPORATE SOURCE: The Institute for Genomic Research, Rockville, MD, 20850, USA
SOURCE: Journal of Bacteriology [illegible], [illegible], [illegible]
CODEN: JOBAAY; ISSN: [illegible]
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Virulence and immunity are poorly understood in Mycobacterium tuberculosis. The complete genome of the M. tuberculosis clin. strain CDC1551 was sequences and a whole-genome comparison with the lab. strain H37Rv performed in order to identify polymorphic sequences with potential relevance to disease pathogenesis, immunity, and evolution. Large-sequence and single-nucleotide polymorphisms were found in numerous genes. Polymorphic loci included a phospholipase C, a membrane lipoprotein, members of an adenylate cyclase gene family, and members of the PE/PPE gene family, some of which have been implicated in virulence or the host immune response. Several gene families, including the PE/PPE gene family, also had significantly higher synonymous and nonsynonymous

substitution frequencies compared to the genome as a whole. A large sample of M. tuberculosis clin. isolates was tested for a subset of the large-sequence and single-nucleotide polymorphisms and widespread genetic variability was found at many of these loci. Phylogenetic and epidemiol. anal. was carried out to investigate the evolutionary relationships among isolates and the origins of specific polymorphic loci. A no. of these polymorphisms appear to have occurred multiple times as independent events, suggesting that these changes may be under selective pressure. Together, these results demonstrate that polymorphisms among M. tuberculosis strains are more extensive than initially anticipated, and genetic variation may have an important role in disease pathogenesis and immunity. The sequence of the clin. strain CDC1551 of M. tuberculosis was deposited in GenBank/EMBL/DDBJ under accession no. AE000516, and the sequence of the genome of the M. tuberculosis lab. strain H37Rv was recently sequenced and deposited as [illegible].

IT **457684-48-9**
RL: BSU (Biological study, unclassified); PRP (Properties); [illegible]
(Biological study)
(amino acid sequence; whole-genome comparison of Mycobacterium tuberculosis clin. and lab. strains)

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 3 OF 26 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:545718 HCAPLUS
DOCUMENT NUMBER: 137:74237
TITLE: The genome of Methanosarcina mazei: evidence for lateral gene transfer between bacteria and Archaea
AUTHOR(S): Deppenmeier, Uwe; Johann, Andre; Hartsch, Thomas; Merkl, Rainer; Schmitz, Ruth A.; Martinez-Arias, Rosa; Henne, Anke; Wiezer, Arnim; Baumer, Sebastian; Jacobi, Carsten; Bruggemann, Holger; Lienard, Tanja; Christmann, Andreas; Bomeke, Mechthild; Steckel, Silke; Bhattacharyya, Anamitra; Lykidis, Athanasios; Overbeek, Ross; Klenk, Hans-Peter; Gunsalus, Robert P.; Fritz, Hans-Joachim; Gottschalk, Gerhard
CORPORATE SOURCE: Gottingen Genomics Laboratory. Department of General Microbiology. Institute of Microbiology and Genetics, Georg-August-University, Goettingen, D-37077, Germany
SOURCE: Journal of Molecular Microbiology and Biotechnology (2002), 4(4), 453-461
CODEN: JMMBFF; ISSN: [illegible]
PUBLISHER: Horizon Scientific Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The Archaeon Methanosarcina mazei and related species are of great ecol. importance as they are the only organisms fermenting acetate, methylamines and methanol to methane, carbon dioxide and ammonia (in case of methylamines). Since acetate is the precursor of 60% of the methane produced on earth these organisms contribute significantly to the prodn. of this greenhouse gas, e.g. in rice paddies. The 4,096,345 base pairs circular chromosome of M. mazei is more than twice as large as the genomes of the methanogenic Archaea currently completely sequenced. There were 3371 open reading frames (ORFs) identified. Based on currently available sequence data 376 of these ORFs are Methanosarcina-specific and 1043 ORFs find their closest homolog in the bacterial domain. About 544 of these ORFs reach significant similarity values only in the bacterial domain. They include [illegible] environmental sensing, gene regulation, [illegible] examples are the occurrence of the bacterial [illegible] system and the presence of tetrahydrofolate-dependent enzymes. These findings might indicate that lateral gene transfer has played an important

evolutionary role in forming the physiol. of this metabolically versatile methanogen. The genome sequence is deposited in GenBank under Accession No. AE008854.

IT **440301-84-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Methanosarcina mazei and evidence for lateral gene transfer between bacteria and archaea

REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITED REFERENCES ARE AVAILABLE IN THE RE FORMAT

L11 ANSWER 4 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:348600 HCAPLUS
DOCUMENT NUMBER: 137:139473
TITLE: Human genome derived single exon nucleic acid probes useful for gene expression analysis
INVENTOR(S): Penn, Sharron Gaynor; Rank, David Russell; Chen, Wenshenq; Hamzel, David Kagen
PATENT ASSIGNEE(S): USA
SOURCE: U.S. Pat. Appl. Publ., 97 pp., Cont.-in-part of U.S. Ser. No. 774,203.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 84
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2002048763	A1	20020425	US 2001-864761	20010523
GB 2360284	A1	20010919	GB 2000-24263	20001004
GB 2360284	B2	20020227		
GB 2361238	A1	20011017	GB 2001-15281	20001004
GB 2361238	B2	20020306		
US 20020081590	A1	20020627	US 2001-774203	20010129
WO 2001057271	A2	20010809	WO 2001-US663	20010130

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WO 2001057271	A2	20010809	WO 2001-US663 20010130
WO 2001057271	A3	20020103	

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WO 2001057275 A2 20010809 WO 2001-US667 20010130

WO 2001057275 C2 20021017

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YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

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WO 2001057275 A2 20010809 WO 2001-US668 20010130

WO 2001057275 A3 20030109

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WO 2001057669 A2 20010809 WO 2001-US669 20010130

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
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BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

[illegible]

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BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
WO 2001066603 A2 20010913 WO 2001-US665 20010130
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
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HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
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SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN,
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BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
US 20020102252 A1 20020801 US 2001-827998 20010406
PRIORITY APPLN. INFO.: US 2000-193312P P 20000204
US 2001-[illegible]P P [illegible]
US 2000-[illegible] A2 [illegible]
US 2000-632366 A2 20000803
US 2000-234657P P 20000921
US 2000-236359P P 20000927
GB 2000-24263 A 20001004
US 2001-774203 A2 20010129
WO 2001-US661 A2 20010130
WO 2001-US662 A2 20010130
WO 2001-US663 A2 20010130
WO 2001-US664 A2 [illegible]
WO 2001-US665 A2 20010130
WO 2001-US666 A2 [illegible]
WO 2001-US667 A2 20010130
WO 2001-US668 A2 20010130
WO 2001-US669 A2 20010130
WO 2001-US670 A2 20010130
TW 2001-[illegible] P [illegible]

AB Methods and app. for predicting, confirming and displaying functional regions from genomic sequence data are used to identify 16,834 unique human genome-derived single exon probes useful for gene expression anal., particularly gene expression anal. by microarray. Also presented are genome-derived single exon microarrays that include such probes, peptides encoded by the exons, and antibodies thereto. The human genome-derived single-exon probes are known to be expressed in one or more human tissues or cell types, particularly human brain, heart, liver, fetal liver,placenta, lung, bone marrow, BT474 and other human mammary epithelial cells, HeLa and other human cervical epithelial cells, and HBL 100 and other human mammary epithelial cells. The invention provides a method of financing, selling and/or licensing genome-derived single-exon microarrays to customer desiring to measure gene expression, comprising: making available for computerized query or subscription service a database having a record corresponding to each genome-derived single exon microarray available for sale and or license. [This abstr. record is one of ten records for this document necessitated by the large no. of index entries required to fully index the [illegible] disclosed in the constraints.].

IT **437115-91-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; human genome derived single exon nucleic acid probes useful for gene expression anal.)

L11 ANSWER 5 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: [illegible] HCAPLUS
DOCUMENT NUMBER: [illegible]
TITLE: complete genome sequence of Methanosarcina acetivorans C2A reveals extensive metabolic and physiological diversity

AUTHOR(S): Galagan, James E.; Nusbaum, Chad; Roy, Anna; Endrizzi, Matthew G.; Macdonald, Peter; FitzHugh, Will; Calvo, Sarah; Engels, Reinhard; Smirnov, Serge; Atnoor, Doron; Brown, Adam; Allen, Nicole; Naylor, Jerome; Stange-Thomann, Nicole; DeArellano, Kurt; Johnson, Robin; Linton, Lauren; McEwan, Paul; McKernan, Kevin; Talamas, Jessica; Tirrell, Andrea; Ye, Wenquan; Zimmer, Andrew; Barber, Robert D.; Cann, Isaac; Graham, David E.; Grahame, David A.; Guss, Adam M.; Heddericb, Reiner; Ingram-Smith, Cheryl; Kuettner, H. Craig; Krzycki, Joseph A.; Leigh, John A.; Li, Weixi; Liu, Jinfeng; Mukhopadhyay, Biswarup; Reeve, John N.; Smith, Kerry; Springer, Timothy A.; Umayam, Lowell A.; White, Owen; White, Robert H.; de Macario, Everly Conway; Ferry, James G.; Jarrell, Ken F.; Jing, Hua; Macario, Alberto J. L.; Paulsen, Ian; Pritchett, Matthew; Sowers, Kevin R.; Swanson, Russell V.; Zinder, Stephen H.; Lander, Eric; Metcalf, William W.; Birren, Bruce

CORPORATE SOURCE: Whitehead Institute/Center for Genome Research, Cambridge, MA, 02141, USA

SOURCE: Genome Research (2002), 12(4), 532-542
CODEN: GEREFS; ISSN: 1088-9051

PUBLISHER: Cold Spring Harbor Laboratory Press

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Methanogenesis, the biol. prodn. of methane, plays a pivotal role in the global carbon cycle and contributes significantly to global warming. The majority of methane in nature is derived from acetate. The complete genome sequence of an acetate-utilizing methanogen, Methanosarcina acetivorans C2A, is now reported. Methanosarcineae are the most metabolically diverse methanogens, thrive in a broad range of environments, and are unique among the Archaea in forming complex multicellular structures. This diversity is reflected in the genome of M. acetivorans. At 5,751,492 base pairs it is by far the largest known archaeal genome. The 4524 open reading frames attest to a surprisingly complex and unanticipated variety of metabolic and cellular capabilities. The presence of novel methyltransferases indicates the likelihood of undiscovered natural energy sources for methanogenesis, whereas the presence of single-subunit carbon monoxide dehydrogenases raises the possibility of nonmethanogenic growth. Although motility has not been obsd. in any Methanosarcineae, a flagellin gene cluster and two complete chemotaxis gene clusters were identified. The availability of genetic methods, coupled with its physiol. and metabolic diversity, makes M. acetivorans a powerful model organism for the study of archaeal biol. The genome sequence is deposited in GenBank under Accession No. AE010656-AE011189.

IT **406874-66-6**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; complete genome sequence of Methanosarcina acetivorans C2A reveals extensive metabolic and physiol. diversity)

REFERENCE COUNT: 58 THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 6 OF 26 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2002:[illegible] HCAPLUS

DOCUMENT NUMBER: 137:[illegible]

TITLE: Functional annotation of a full-length Arabidopsis cDNA collection

AUTHOR(S): [illegible]

Miramatsu, Masami; Hayashizaki, Yoshihide; Kawai, Jun;
Carninci, Piero; Itoh, Masayoshi; Ishii, Yoshiyuki;
Arakawa, Takahiro; Shibata, Kazuhiro; Shinagawa,
Akira; Shimotohno, Kunio

CORPORATE SOURCE: Plant Molecular Engineering Team, Plant Functional
Genomics Res. Group, RIKEN Genomic Sciences Center
, 1-1-1 Koyadai, Tsukuba, 3 , Japan

SOURCE: Science (Washington, D. C., United States) ,
(), 141-148
CODEN: SCIEAS; ISSN:

PUBLISHER: American Association for the Advancement of Science

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Full-length cDNAs are essential for the correct annotation of genomic sequences and for the functional anal. of genes and their products. About 155,144 RIKEN Arabidopsis full-length (RAFL) cDNA clones were isolated. The 3'-end expressed sequence tags (ESTs) of 155,144 RAFL cDNAs were clustered into 14,668 nonredundant cDNA groups, about 60% of predicted genes. 5'-ESTs were also obtained from 14,334 nonredundant cDNA groups and a promoter database constructed. The sequence database of the RAFL cDNAs is useful for promoter anal. and correct annotation of predicted transcription units and gene products. Furthermore, the full-length cDNAs are useful resources for analyses of the expression profiles, functions, and structures of plant proteins. [This abstr. record is one of sixteen records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **437141-30-5**
RL: BSU (Biological study, unclassified); PRP (Properties); RCT (Reactant)
Biological study
(amino acid sequence; full-length cDNA collection of a full-length Arabidopsis cDNA collection)

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 7 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:173757 HCAPLUS
DOCUMENT NUMBER: 136:351357
TITLE: Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human adult liver
INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng; Rank, David R.
PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
SOURCE: PCT Int. Appl., 659 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 84
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO [illegible]	A2	[illegible]	WO [illegible]-US[illegible]	[illegible]

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
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GB [illegible] A1 [illegible] [illegible] [illegible]

AU [illegible]
GB 2361238 A1 20011017 GB 2001-15291 20010604
GB 2361238 B2 20020306
WO [illegible] A2 20011018 WO 2001-US664 20010130
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
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SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
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BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
[illegible] A1 [illegible]
PRIORITY APPLN. INFO.:
[illegible]
US 2000-236359P P 20000927
GB 2000-24263 A 20001004
WO 2001-US664 A 20010130

AB A single exon nucleic acid microarray comprising 13,109 single exon nucleic acid probes for measuring gene expression in a sample derived from human adult liver is described. These unique exons are within longer probe sequences; sequencing confirms the exact chem. structure of each probe. Some amplicons have more than one exon, and some exons are contained in more than one amplicon. Expression, homol., and functional information are provided for the genome-derived single exon probes that are expressed significantly in human adult liver cells. Also described are 12,836 single exon nucleic acid probes and 12,583 proteins expressed in the adult liver and their use in methods for detecting gene expression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a genomic DNA sequence, and for assigning exons to a single gene.

IT **420924-39-6**
RL: ANT (Analyte); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human adult liver)

L11 ANSWER 6 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:157797 HCAPLUS
DOCUMENT NUMBER: 136:195341
TITLE: Cloning and cDNA and deduced amino acid sequences of 21 human secreted proteins
INVENTOR(S): Rosen, Craig A.; Komatsoulis, George A.; Baker, Kevin P.; Birse, Charles E.; Soppet, Daniel R.; Olsen, Henrik S.; Moore, Paul A.; Wei, Ping; Ruben, Steven; Park, L. Sukhan; Shi, Tasso; Li, Y. H.; Piccoli, Michele; Ni, Jian
PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA
SOURCE: PCT Int. Appl., 184 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

[illegible]

AB The present invention relates to 21 novel human secreted proteins and isolated nucleic acids [illegible] the coding regions of the genes encoding such proteins. Tissue distribution, sequence homologies, and preferred epitope sites are provided for the secreted proteins, as well as chromosomal mapping of some of the genes. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins in bacterial, insect, and mammalian cells. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins. High-throughput screening assays are also provided for various putative activities of the secreted proteins.

IT **400696-91-5P**
RL: BPN (Biosynthetic preparation); BST (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; cloning and DNA and deduced amino acid sequences of 21 human secreted proteins)

REFERENCE COUNT: 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 9 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:125123 HCAPLUS
DOCUMENT NUMBER: 136:141954
TITLE: Genome sequence of the plant pathogen Ralstonia solanacearum
AUTHOR(S): Salanoubat, M.; Genin, S.; Artiguenave, F.; Gouzy, J.; Mangenot, S.; Arlat, M.; Billault, A.; Brottier, P.; Camus, J. C.; Cattolico, L.; Chandler, M.; Choisne, N.; Claudel-Renard, C.; Cunnac, S.; Demange, N.; Gaspin, C.; Lavie, M.; Moisan, A.; Robert, C.; Saurin, W.; Schiex, T.; Siguier, P.; Thebault, P.; Whalen, M.; Wincker, P.; Levy, M.; Weissenbach, J.; [illegible]
CORPORATE SOURCE: [illegible]
SOURCE: Nature [illegible], United Kingdom [illegible], 415(6871), 497-502
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Nature Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Ralstonia solanacearum is a devastating, soil-borne plant pathogen with a global distribution and an unusually wide host range. It is a model system [illegible] the [illegible] mechanisms governing pathogenicity. The complete genome sequence and its anal. of strain GMI1000 is presented. The 5.8-megabase (Mb) genome is organized into two replicons: a 3.7-Mb chromosome and a 2.1-Mb megaplasmid. Both replicons have a mosaic structure providing evidence for the acquisition of genes through horizontal gene transfer. Replicons carry genetically mobile elements associd. with the presence of G+C bias may have an important function in genome evolution. The [illegible] genes may provide [illegible] with a role in pathogenicity. [illegible]

factors were identified. The complete repertoire of type III secreted effector proteins can be studied. Over 40 candidates were identified. Comparison with other genomes suggests that bacterial plant pathogens and animal pathogens harbor distinct arrays of specialized type III-dependent effectors.

IT 394342-70-2 394342-96-2
RL: BSU (Biological study, unclassified ; PRP (Properties'; RIOL (Biological study)
(amino acid sequence; genome sequence of the plant pathogen Ralstonia solanacearum)

REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 1 OF [illegible] ON STN
ACCESSION NUMBER: [illegible]
DOCUMENT NUMBER: [illegible]
TITLE: Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human placenta
INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng; Rank, David R.
PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
SOURCE: PCT Int. Appl., 654 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 84
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001057272	A2	20010809	WO 2001-US663	20010130
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
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GB 2360284	A1	20010919	GB 2000-24263	20001004
GB 2360284	B2	20020227		
GB 2361238	A1	20011017	GB 2001-15281	20001004
GB 2361238	B2	20020306		
WO 2001057272	A2	20010809	WO 2001-US663	20010130
WO 2001057272	A3	20030123		
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RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
US [illegible]	A1	[illegible]	[illegible]	[illegible]

PRIORITY APPLN. INFO.:

[illegible]

[illegible]
WO [illegible] A [illegible]

AB A single exon nucleic acid microarray comprising 13,[illegible] single exon nucleic acid probes for measuring gene expression in a sample derived from human placental cells is described. These single exon nucleic acid probes sequences; sequences [illegible] gene. [illegible] gene. [illegible] contained in more than one amplicon. Expression information are provided for the genome-derived single exon probes that are expressed significantly in human placenta. Also described are 13,[illegible] single exon nucleic acid probes and 12,000 proteins expressed in the placenta cells and their use in methods for detecting gene expression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exons to a single gene. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **400664-75-7**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human placenta)

L11 ANSWER 11 OF [illegible] HCAPLUS [illegible]
ACCESSION NUMBER: [illegible] HCAPLUS
DOCUMENT NUMBER: 136:198264
TITLE: Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver
INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng; Rank, David R.
PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
SOURCE: PCT Int. Appl., 639 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 84
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO [illegible]	A2	[illegible]	WO [illegible]-[illegible]	[illegible]
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			
RW:	GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG			
GB [illegible]	A1	20010919	GB 2000-24263	20001004
GB [illegible]	B2	[illegible]		
GB [illegible]	A1	20011017	GB 2001-15291	20001004
GB [illegible]	B2	[illegible]		
WO [illegible]	A2	[illegible]	WO 2001-US664	20010101
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM			

PN: [illegible]

PRIORITY APPLN. INFO.:

AB A single exon nucleic acid microarray comprising 1,[illegible] single exon nucleic acid probes for measuring gene expression in a sample derived from human fetal liver cells is described. These unique exons are within longer probe sequences; sequencing confirms the exact size, structure of each probe. Some amplicons have more than one exon, and some exons are contained in more than one amplicon. Expression, homol., and functional information are provided for the non-redundant single exon probes that are expressed significantly in human fetal liver cells. Also described are 12,456 single exon nucleic acid probes and 12,027 proteins expressed in the fetal liver and their use in methods for detecting gene expression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exons to a single gene. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **400957-73-5**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human fetal liver)

L11 ANSWER 12 OF 26 HCAPLUS COPYRIGHT [illegible] ACS
ACCESSION NUMBER: [illegible] HCAPLUS
DOCUMENT NUMBER: [illegible]
TITLE: Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain
INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng; Rank, David R.
PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
SOURCE: PCT Int. Appl., 650 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 64
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO [illegible]	A2	[illegible]	WO [illegible]	[illegible]

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

EP [illegible] A1 [illegible] EP [illegible] [illegible]
US [illegible] A1 [illegible]

PRIORITY APPLN. INFO.:

US 2000-608408 A 20000630
US 2000-632366 A 20000803
US 2000-634697P P 20000921
US 2000-636359P P 20000927

AB A single exon nucleic acid microarray comprising 12,821 single exon nucleic acid probes for measuring gene expression in a sample derived from human brain cells is described. These unique exons are within longer probe sequences; sequencing confirms the exact chem. structure of each probe. Some amplicons have more than one exon, and some exons are contained in more than one amplicon. Expression, homol., and functional information are provided for the genome-derived single exon probes that are expressed significantly in human brain. Also described are 12,613 single exon nucleic acid probes and 12,377 proteins expressed in the brain and their use in methods for detecting gene expression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exons to a single gene. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **412969-90-5**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human brain)

L11 ANSWER 13 OF 20 HCAPLUS COPYRIGHT 2004 ACS
ACCESSION NUMBER: 2001:11[illegible]
DOCUMENT NUMBER: 13[illegible]
TITLE: Human [illegible]-exon nucleic acid probes useful for analysis of gene expression in human bone marrow
INVENTOR(S): Penn, Sharron G.; Hanzel, David K.; Chen, Wensheng; Rank, David R.
PATENT ASSIGNEE(S): Molecular Dynamics, Inc., USA
SOURCE: PCT Int. Appl., [illegible] pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 84
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO [illegible]	A1	[illegible]	WO [illegible]	[illegible]

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

GB 2361244 A1 [illegible] GB 2000-24263 20001004
GB 2360284 B2 20020227
GB 2361238 A1 [illegible] GB 2001-[illegible] [illegible]
GB 2361238 B2 [illegible]
WO 2001057276 A2 [illegible] WO [illegible] [illegible]
WO 2001057276 A3 [illegible]

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN,
YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

US [illegible] A1 [illegible] US 2001-[illegible] [illegible]

PRIORITY APPLN. INFO.:
US 2000-180312P P 20000204
US 2000-207456P P 20000526
US 2000-608408 A 20000630
US 2000-632366 A 20000803
US 2000-234687P P 20000921
US 2000-236359P P 20000927
GB 2000-24263 A 20001004
WO 2001-US669 A [illegible]

AB A single exon nucleic acid microarray comprising [illegible] single exon nucleic acid probes for measuring gene expression in a sample derived from human bone marrow is described. These unique exons are within longer probe sequences; sequencing confirms the exact chem. structure of each probe. Some amplicons have more than one exon, and some exons are contained in more than one amplicon. Expression, homol., and functional information are provided for the genome-derived single exon probes that are expressed significantly in human bone marrow. Also described are 12,898 single exon nucleic acid probes and 12,[illegible] proteins expressed in the bone marrow and their use in methods for detecting gene expression. The genome-derived single exon nucleic acids comprise a novel type of nucleic acid microarray for verifying gene expression. In addn., methods are provided for identifying exons in a eukaryotic genome, and for assigning exons to a single gene. [This abstr. record is one of nine records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **402671-83-4**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study)
(amino acid sequence; human genome-derived single exon nucleic acid probes useful for anal. of gene expression in human bone marrow)

L11 ANSWER 14 OF [illegible] HCAPLUS COPYRIGHT [illegible] ACS
ACCESSION NUMBER: [illegible]
[illegible]
DOCUMENT NUMBER: [illegible]
[illegible]
TITLE: Human nucleic acids and their encoded proteins and antibodies
INVENTOR(S): Rosen, Craig A.; Barash, Steven C.; Ruben, Steven M.

PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA
SOURCE: PCT Int. Appl., [illegible] pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: [illegible]
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001053367	A1	[illegible]	WO 2001-[illegible]	[illegible]
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2001041413	A5	20010807	AU 2001-41413	20010117
AU 2001041416	A5	20010807	AU 2001-41416	20010117
AU 2001041417	A5	20010807	AU 2001-41417	20010117
AU 2001050770	A5	20010807	AU 2001-50770	20010117
US 2002042096	A1	20020411	US 2001-[illegible]	20010117
US 2002077270	A1	20020620	US 2001-[illegible]	20010117
US 2002086811	A1	20020704	US 2001-[illegible]	[illegible]
US [illegible]	A1	[illegible]	[illegible]	[illegible]
US 2002086821	A1	20020704	US 2001-[illegible]	[illegible]
US 2002086822	A1	20020704	US 2001-764886	20010117
US 2002086823	A1	20020704	US 2001-764889	20010117
US 2002086330	A1	20020704	US 2001-764893	20010117
US 2002090615	A1	20020711	US 2001-764878	20010117
US 2002090674	A1	20020711	US 2001-764903	20010117
US 2002094953	A1	20020718	US 2001-764860	20010117
US 2002102638	A1	20020801	US 2001-764846	20010117
US 2002119919	A1	20020829	US 2001-764855	20010117
US 2002132767	A1	20020919	US 2001-764847	20010117
US 2002147140	A1	20021010	US 2001-764877	20010117
US 2002151479	A1	20021017	US 2001-764873	20010117
US 2002161208	A1	20021031	US 2001-764884	20010117
US 2002164685	A1	20021107	US 2001-764857	20010117
US 2002173454	A1	20021121	US 2001-764904	20010117
EP 1261703	A1	20021204	EP 2001-912655	[illegible]
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
AU 2001052878	A5	[illegible]	AU 2001-[illegible]	[illegible]
AU 2001043137	A5	20010814	AU 2001-43137	[illegible]
US 2003013649	A1	[illegible]	US 2001-[illegible]	[illegible]

PRIORITY APPLN. INFO.:

US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
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US [illegible]	P	[illegible]
US [illegible]	P	[illegible]

US 2000-217486P	P	20000711
US 2000-218291P	P	20000714
US 2000-221363P	P	20000726
US 2000-221364P	P	20000726
US 2000-224513P	P	20000814
US 2000-224514P	P	20000814
US 2000-225213P	P	20000814
US 2000-225214P	P	20000814
US 2000-225266P	P	20000814
US 2000-225267P	P	20000814
US 2000-225268P	P	20000814
US 2000-2252[illegible]P	P	2000[illegible]14
US [illegible]	P	[illegible]14
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US [illegible]	P	[illegible]14
US [illegible]	P	[illegible]14
US 2000-226274P	P	20000818
US 2000-226661P	P	20000822
US 2000-226664P	P	20000822
US 2000-227162P	P	20000822
US 2000-227504P	P	20000823
US 2000-228924P	P	20000831
US 2000-229343P	P	20000901
US 2000-229344P	P	20000901
US 2000-229287P	P	20000901
US 2000-229345P	P	20000901
US 2000-229509P	P	20000905
US 2000-229513P	P	20000905
US 2000-231413P	P	20000908
US 2000-234223P	P	20000921
US 2000-234274P	P	20000921
US 2000-234997P	P	20000925
US 2000-235834P	P	20000927
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US 2000-236368P	P	20000929
US 2000-236369P	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US 2000-237039P	P	20001002
US 2000-237040P	P	20001002
US 2000-241785P	P	20001020
US 2000-241809P	P	20001020
US 2000-244617P	P	20001101
US 2000-246478P	P	20001108
US 2000-246523P	P	20001108
US 2000-246524P	P	20001108
US 2000-246609P	P	20001108
US 2000-246613P	P	20001108
US 2000-249207P	P	20001117
US 2000-249208P	P	20001117
US 2000-249209P	P	20001117
US 2000-249210P	P	20001117
US 2000-249211P	P	20001117
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
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US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]

US	2000-249263P	P	20001117
US	2000-249264P	P	20001117
US	2000-249265P	P	20001117
US	2000-249297P	P	20001117
US	2000-249299P	P	20001117
US	[illegible]	P	[illegible]
[illegible]			
US	[illegible]	P	[illegible]
US	2000-256719P	P	20001205
US	2000-251479P	P	20001206
US	2000-251856P	P	20001208
US	2000-251868P	P	20001208
US	2000-251869P	P	20001208
US	2000-251990P	P	20001209
US	2001-764863	B1	20010117
WO	2001-US1338	W	20010117

AB The present invention relates to novel musculoskeletal system-related polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "musculoskeletal system antigens", and the use of such musculoskeletal system antigens for detecting disorders of the musculoskeletal system, particularly the presence of cancer and cancer metastases. More specifically, 1023 isolated musculoskeletal system-assocd. cDNA mols. are provided encoding novel musculoskeletal system-assocd. polypeptides. Novel musculoskeletal system polypeptides and antibodies that bind to these polypeptides are provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing human musculoskeletal system assocd. polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders related to the musculoskeletal system, including cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or compns. for inhibiting the prodn. and function of the polypeptides of the present invention.

IT **384873-95-4P**
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; human musculoskeletal system-specific nucleic acids and their encoded proteins and antibodies)

L11 ANSWER 15 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:763025 HCAPLUS
DOCUMENT NUMBER: 136:336111
TITLE: Albumin fusion proteins with therapeutic proteins for improved shelf-life
INVENTOR(S): Rosen, Craig A.; Haseltine, William A.
PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA
SOURCE: PCT Int. Appl., [illegible] pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: [illegible]
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO [illegible]	A1	[illegible]	WO 2001-US1338	20010117

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM,

AB The present invention encompasses fusion proteins of albumin with various therapeutic proteins. Therapeutic proteins may be stabilized to extend the shelf-life, and/or to retain the therapeutic protein's activity for extended periods of time in soln., in vitro and/or in vivo, by genetically or chem. fusing or conjugating the therapeutic protein to all or a fragment or variant of albumin. The albumin fusion proteins may also reduce the need to formulate the protein soln. with large excesses of carrier proteins to prevent loss of therapeutic proteins due to factors such as binding to the container. Nucleic acid mols. encoding the albumin fusion proteins of the invention are also encompassed by the invention, as are vectors contg. these nucleic acids, host cells transformed with these nucleic acids vectors, and methods of making the albumin fusion proteins of the invention and using these nucleic acids, vectors, and/or host cells. Thus, plasmid vectors are constructed in which DNA encoding the desired therapeutic protein may be inserted for expression of the albumin fusion proteins in yeast (pPPC0005) and mammalian cells (pC4:HSA). Yeast-derived signal sequences from Saccharomyces cerevisiae invertase SUC2 gene, or the stanniocalcin or native human serum albumin signal peptides, are used for secretion in yeast or mammalian systems, resp. Thus, the fusion product of human growth hormone with residues 1-387 of human serum albumin retains essentially intact biol. activity after 5 wk of incubation in tissue culture media at 37.degree., whereas recombinant human growth hormone is used as control lost the biol. activity in the first week. Although the potency of the albumin fusion proteins is slightly lower than the unfused counterparts in rapid bioassays, their biol. stability results in much higher biol. activity in the longer term in vitro assay or in vivo assays. Addnl., the present invention encompasses pharmaceutical compns. comprising albumin fusion proteins and methods of treating, preventing, or ameliorating diseases, disorders or conditions using albumin fusion proteins of the invention.

IT **369644-05-3**
RL: PRP (Properties)
(unclaimed protein sequence; albumin fusion proteins with therapeutic proteins for improved shelf-life)

REFERENCE COUNT: 3 THERE ARE 3 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 16 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:[illegible] HCAPLUS
DOCUMENT NUMBER: 135:[illegible]
TITLE: Nucleic acids and their encoded polypeptides from human kidney marrow
INVENTOR(S): Ford, John E.; Boyle, Bryan J.; Tang, Y. Tom; Liu, Chenghua; Asundi, Vinod; Chen, Ping; Nam, Albert J.; Ren, Feiyan; Drmanac, Radoje T.
PATENT ASSIGNEE(S): Hyseq, Inc., USA
SOURCE: PCT Int. Appl., [illegible] pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent

LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001-US3782	A1	20010816	WO 2001-US3782	20010205
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW:	AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
AU 2001034847	A5	20010814	AU 2001-34847	20010205

PRIORITY APPLN. INFO.:
US 2000-496914 A 20000203
US 2000-598075 A 20000620
US 2000-620325 A 20000719
US 2000-250583P P 20001130
WO 2001-US3782 W 20010205

AB The present invention provides a collection or library of 94 nucleic acid contig sequences assembled from expressed sequence tag or cDNA libraries isolated mainly by sequencing by hybridization (SBH), std. PCR, Sanger sequencing techniques, and in some cases, sequences obtained form one or more public databases. The cDNA libraries are from human bone marrow sources and nearest neighbor sequence homol. plus are provided. The invention also relates to the proteins encoded by said nucleic acids, along with therapeutic, diagn. and research uses for the polynucleotides and proteins.

IT **353568-97-5 354113-34-1**
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; nucleic acids and their encoded polypeptides from human bone marrow)

L11 ANSWER 17 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:566854 HCAPLUS
DOCUMENT NUMBER: 135:163414
TITLE: Human nucleic acids and their encoded proteins and antibodies
INVENTOR(S): Rosen, Craig A.; Barash, Steven C.; Ruben, Steven M.
PATENT ASSIGNEE(S): Human Genome Sciences, Inc., USA
SOURCE: PCT Int. Appl., 511 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 40
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001058944	A2	20010816	WO 2001-US3782	20010205
W:	AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

AT [illegible]	A1	[illegible]	AT 2001-50[illegible]	2001011[illegible]
US 2002[illegible]	A1	2002[illegible]	US 2001-764[illegible]	[illegible]
US 2002[illegible]	A1	[illegible]	US 2001-764[illegible]	[illegible]
US [illegible]	A1	[illegible]	US 2001-764[illegible]	[illegible]
US 2002[illegible]	A1	2002[illegible]	US 2001-764[illegible]	2001011[illegible]
US 2002[illegible]	A1	2002[illegible]	US 2001-764881	20010117
US 2002[illegible]	A1	20020704	US 2001-764886	20010117
US 2002[illegible]	A1	20020704	US 2001-764889	20010117
US 2002[illegible]330	A1	20020704	US 2001-764893	20010117
US 2002090615	A1	20020711	US 2001-764878	20010117
US 2002090674	A1	20020711	US 2001-76490[illegible]	20010117
US 2002[illegible]	A1	[illegible]	US 2001-764[illegible]	[illegible]
US [illegible]	A1	[illegible]	US [illegible]	[illegible]
US 2002[illegible]	A1	[illegible]	US 2001-764[illegible]	[illegible]
US 2002132767	A1	2002091[illegible]	US 2001-764[illegible]	[illegible]
US 2002147140	A1	2002101[illegible]	US 2001-76487[illegible]	20010117
US 2002151479	A1	2002101[illegible]	US 2001-7648[illegible]	20010117
US 2002161[illegible]	A1	[illegible]	US 2001-7648[illegible]	20010117
US 200216468[illegible]	A1	2002111[illegible]	US 2001-76488[illegible]	20010117
EP 1255869	A1	20021113	EP 2001-916067	20010117

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR

US 2002173454	A1	20021121	US 2001-764904	20010117
US 2002165137	A1	20021107	US 2001-860670	20010521
US 2003013649	A1	20030116	US 2001-989442	20011121

PRIORITY APPLN. INFO.:

US 2000-179065P	P	20000131
US 2000-180628P	P	20000204
US 2000-205515P	P	20000519
US 2000-216880P	P	20000707
US 2000-218290P	P	20000714
US 2000-225447P	P	20000814
US 2000-229343P	P	20000901
US 2000-230437P	P	20000906
US 2000-231243P	P	20000908
US 2000-234997P	P	2000092[illegible]
US 2000-236367P	P	[illegible]
US [illegible]	P	[illegible]
US 2000-24[illegible]	P	[illegible]
US 2000-24[illegible]	P	[illegible]
US 2000-246525P	P	20001108
US 2000-246526P	P	20001108
US 2000-246528P	P	20001108
US 2000-249210P	P	20001117
US 2000-249211P	P	20001117
US 2000-249214P	P	20001117
US 2000-249265P	P	20001117
US 2000-250160P	P	20001201
US 2000-250391P	P	20001201
US 2000-251030P	P	20001205
US 2000-251988P	P	20001205
US 2000-256719P	P	20001205
US 2000-251479P	P	20001206
US 2000-251869P	P	2000120[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US 2000-[illegible]63P	P	[illegible]

US	2000-[illegible]P	P	[illegible]
US	2000-[illegible]P	P	[illegible]
US	2000-[illegible]P	P	[illegible]
US	2000-[illegible]P	P	[illegible]
US	2000-228168P	P	20000814
US	2000-228258P	P	20000814
US	2000-228757P	P	20000814
US	2000-228758P	P	20000814
US	2000-228868P	P	20000822
US	2000-228924P	P	20000830
US	2000-229287P	P	20000901
US	2000-229344P	P	20000901
US	2000-229345P	P	20000901
US	2000-229509P	P	20000905
US	2000-229513P	P	20000905
US	2000-231413P	P	20000908
US	2000-234223P	P	20000911
US	2000-234274P	P	20000911
US	2000-235834P	P	20000914
US	2000-[illegible]P	P	[illegible]
US	[illegible]	[illegible]	[illegible]
US	2000-[illegible]P	P	[illegible]
US	2000-236369P	P	20000914
US	2000-236370P	P	20000914
US	2000-236802P	P	20001102
US	2000-237057P	P	20001102
US	2000-237058P	P	20001102
US	2000-237059P	P	20001102
US	2000-237060P	P	20001102
US	2000-241786P	P	20001030
US	2000-241809P	P	20001030
US	2000-244617P	P	20001101
US	2000-249299P	P	20001107
US	2000-251866P	P	20001208
US	2000-251868P	P	20001208
US	2000-251869P	P	20001208
US	2001-764859	A2	20010117
US	2001-764865	B1	20010117
WO	2001-US1546	W	20010117

AB The present invention relates to novel human polynucleotides and the polypeptides encoded by these polynucleotides, and the use of such polypeptides for detecting disorders. More specifically, 79 isolated human cDNA mols. are provided encoding novel polypeptides. Antibodies that bind to these polypeptides are also provided. Also provided are vectors, host cells, and recombinant and synthetic methods for producing the novel human polynucleotides and/or polypeptides. The invention further relates to diagnostic and therapeutic methods useful for diagnosing, treating, preventing and/or prognosing disorders and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of polynucleotides and polypeptides of the invention. The present invention further relates to methods and/or comprs. for inhibiting the prodn. and function of the polypeptides of the present invention.

IT **353554-69-5**, Protein (human clone HFIEC13)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
protein sequences; human nucleic acids and their encoded proteins and antibodies)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 10 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:397059 HCAPLUS
DOCUMENT NUMBER: 135:13431
TITLE: [illegible]

TITLE: Enzymes in the synthesis of polyunsaturated fatty acids and lipids
INVENTOR(S): Lerchl, Jens; Renz, Andreas; Ehrhardt, Thomas; Reindl, Andreas; Cirpus, Petra; Bischoff, Friedrich; Frank, Markus; Frenck, Anette; Duwenig, Elke; Schmidt, Ralf-Michael; Broer, Ralf
PATENT ASSIGNEE(S): Basf Plant Science Gmbh, Germany
SOURCE: PCT Int. Appl., 115 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001038541	A1	20010531	WO 1999-EP9108	19991125
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2001017045	A5	20010604	AU 2001-17045	20001122
BR 2000015905	A	20020806	BR 2000-15905	20001122
EP 1282713	A2	20030212	EP 2000-979617	20001122
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				

PRIORITY APPLN. INFO.: WO 1999-EP9108 W 19991125
WO 2000-EP11615 W 20001122

AB Isolated nucleic acid mols., designated LMRP nucleic acid mols., which encode novel LMRPs from e.g. Physcomitrella patens are described. The invention also provides antisense nucleic acid mols., recombinant expression vectors contg. LMRP nucleic acid mols., and host cells into which the expression vectors have been introduced. The invention sill further provides isolated LMRPs, mutated LMRPs, fusion proteins, antigenic peptides and methods for the improvement of the prodn. of a desired compd. from transformed cells, organisms or plants based on genetic engineering of LMRP genes in these organisms.

IT 343286-49-7
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; genes of Physcomitrella patens encoding homologs of enzymes of synthesis of polyunsatd. fatty acids and lipids)

REFERENCE COUNT: THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 2 OF 2 HCAPLUS COPYRIGHT 2004 ACS
ACCESSION NUMBER: 2001:[illegible]
DOCUMENT NUMBER: 135:[illegible]
TITLE: Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis
INVENTOR(S): Alexandrov, Nikolai; Brover, Vyacheslav; Chen, Nianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Lianshen; Dumas, J.

PATENT ASSIGNEE(S): [illegible] Inc., USA
SOURCE: Eur. Pat. Appl., [illegible] pp.
CODEN: [illegible]
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: [illegible]
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1133[illegible]	A2	20000906	EP 2000-301439	20000225
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2300692	AA	20000825	CA 2000-2300692	20000225
CA 2302[illegible]	AA	20001006	CA 2000-2302[illegible]	20000406
EP [illegible]	A2	[illegible]	EP [illegible]	[illegible]
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1054060	A2	20001122	EP 2000-314161	20000517
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.:

US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US 1999-146389P	P	19990602
US 1999-147038P	P	19990803
US 1999-147204P	P	19990804
US 1999-147302P	P	19990804
US 1999-147192P	P	19990805
US 1999-147260P	P	19990805
US 1999-147303P	P	19990806
US 1999-147416P	P	19990806
US 1999-147493P	P	19990809
US 1999-147935P	P	19990809
US 1999-148171P	P	19990810
US 1999-148319P	P	19990811
US 1999-148341P	P	19990812
US 1999-148565P	P	19990813
US 1999-14[illegible]P	P	19990813
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	19990325
US 1999-126[illegible]P	P	19990329
US 1999-127402P	P	19990401
US 1999-128234P	P	19990406
US 1999-128714P	P	19990408
US 1999-129845P	P	19990416
US 1999-130[illegible]P	P	19990419
US 1999-130449P	P	19990421
US 1999-130510P	P	19990423
US 1999-130891P	P	19990423
US 1999-131449P	P	19990428
US 1999-132048P	P	19990430
US 1999-132[illegible]P	P	19990430
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]
US [illegible]	P	[illegible]

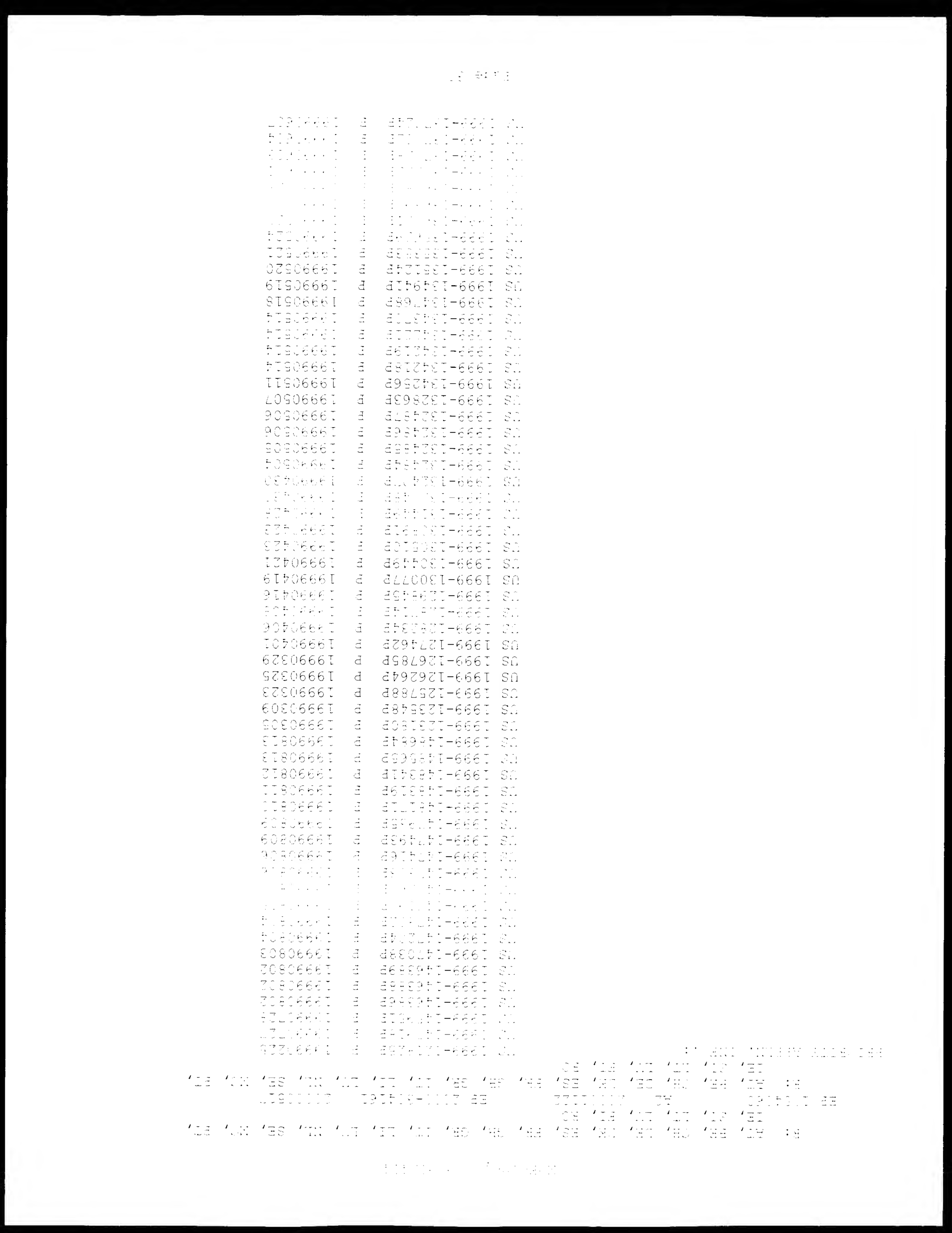
US	1999-134218P	P	19990514
US	1999-134219P	P	19990514
US	1999-134221P	P	19990514
US	1999-134370P	P	19990514
US	1999-134768P	P	19990518
US	1999-134941P	P	19990519
US	1999-135104P	P	19990521
US	1999-135105P	P	19990521
US	1999-135106P	P	19990521
US	1999-136042P	P	19990521
US	1999-136741P	P	19990525
US	1999-137222P	P	19990601
US	1999-137528P	P	19990603
US	1999-137602P	P	19990604
US	1999-137724P	P	19990607
US	1999-138094P	P	19990608

AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #35A19) and Arabidopsis thaliana (ecotype Wassilewski), and polypeptides encoded thereby. The DNA mols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence or as an UTR or as a 3' termination sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present expt., but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to CA133:162185280 necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **302645-65-4 302645-66-5**
FL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; sequence-detd. DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)

L11 ANSWER 20 OF 26 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:754707 HCAPLUS
DOCUMENT NUMBER: 133:318296
TITLE: Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis
INVENTOR(S): Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.
PATENT ASSIGNEE(S): Ceres Inc., USA
SOURCE: Eur. Pat. Appl., 339 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 16
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1033405	A2	20000906	EP 2000-301439	20000225
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2300692	AA	20000825	CA 2000-2300692	20000225
CA 2302928	AA	20000926	CA 2000-2302928	20000326
EP 1038729	A2	20000927	EP 2000-303770	20000504



AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays HYBRID SEED #35A14 and Arabidopsis thaliana (ecotype Wassilewskij, and polypeptides encoded thereby. The DNA mols. are useful for [illegible] gene in the organism, in [illegible] tools for genetic mapping, for studying [illegible] DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present expt., but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of carrot cells. [This abstr. record is one of 15 records supplemental to [illegible], in which fully the large no. of index entries required to fully index the document and publication system constraints.].

IT **302411-42-3 302411-43-4**
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis)

L11 ANSWER 21 OF 26 HCAPLUS COPYRIGHT [illegible] ACS
ACCESSION NUMBER: [illegible]
DOCUMENT NUMBER: 131:31634
TITLE: Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and Arabidopsis
INVENTOR(S): Alexandrov, Nickolai; Brover, Vyacheslav; Chen, Xianfeng; Subramanian, Gopalakrishnan; Troukhan, Maxim E.; Zheng, Liansheng; Dumas, J.
PATENT ASSIGNEE(S): Ceres Inc., USA
SOURCE: Eur. Pat. Appl., 239 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 16
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1033405	A2	[illegible]	EP 2000-301439	[illegible]
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
CA 2300692	AA	[illegible]	CA 2000-2300692	[illegible]
CA 2302328	AA	[illegible]	CA 2000-2302328	[illegible]
EP 1057728	A2	[illegible]	EP 2000-301771	[illegible]
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
EP 1054060	A2	[illegible]	EP 2000-111161	[illegible]
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				

PRIORITY APPLN. INFO.:

US	[illegible]	P	[illegible]
US	1999-145891P	P	19990727
US	1999-145951P	P	19990728
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]
US	[illegible]	P	[illegible]

US 1999-126264P P 19990325
US 1999-126785P P 19990329
US 1999-127462P P 19990401
US 1999-128234P P 19990406
US 1999-128714P P 19990408
US 1999-129545P P 19990416
US 1999-130077P P 19990419
US 1999-130449P P 19990421
US 1999-130510P P 19990423
US 1999-130891P P 19990423
US 1999-131449P P 19990428
US 1999-132048P P 19990430
US 1999-132407P P 19990430
US 1999-132863P P 19990507
US 1999-134256P P 19990511
US 1999-134218P P 19990514
US 1999-134219P P 19990514
US 1999-134221P P 19990514
US 1999-134370P P 19990514
US 1999-134941P P 19990519
US 1999-135124P P 19990520
US 1999-135353P P 19990521
US 1999-135629P P 19990524
US 1999-136021P P 19990525
US 1999-136392P P 19990527
US 1999-136782P P 19990528
US 1999-137222P P 19990601
US 1999-136194P P 19990608

AB The present invention provides DNA mols. that constitute fragments of the genome and cDNAs from Zea mays mays (HYBRID SEED #38A1M) and Arabidopsis thaliana (ecotype Wassilewskij), and polypeptides encoded thereby. The DNA mols. are useful for specifying a gene product in cells, either as a promoter or as a protein coding sequence, or as the DNA in a transcription sequence, and are also useful in controlling the behavior of a gene in the chromosome, in controlling the expression of a gene or as tools for genetic mapping, recognizing or isolating identical or related DNA fragments, or identification of a particular individual organism, or for clustering of a group of organisms with a common trait. Arabidopsis DNA is used in the present exp., but the procedure is a general one. Protocols are provided for Southern hybridizations and transformation of target cells. [This abstr. record is one of 11 records supplemental to CA131:1 publication, necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT 301564-26-1 301564-27-2
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; sequence-detd. DNA fragments and corresponding encoded polypeptides from Brn and Arabidopsis)

L11 ANSWER 22 OF 26 HCAPLUS COPYRIGHT 2008 ACS
ACCESSION NUMBER: [illegible] HCAPLUS
DOCUMENT NUMBER: 134:[illegible]
TITLE: Cloning and expression of a gene encoding a putative chloroplast .omega.6 fatty acid desaturase of marine Chlamydomonas
AUTHOR(S): Miyashita, Hitoshi; Tanaka, Satoshi; Kanaki, Hara...
CORPORATE SOURCE: Tech. Res. Dept., The Kansai Electric Power Co., Inc., Hakushi, Amagasaki, Hyogo, [illegible], Japan
SOURCE: Plant Biotechnology (Tokyo, [illegible])
CODEN: PBIOF9; ISSN: 1342-4580
PUBLISHER: Japanese Society for Plant Cell and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A cDNA encoding putative chloroplast .omega.6 fatty acid desaturase was isolated from a cDNA library of marine Chlamydomonas sp. strain W-80. The mRNA level of this gene under various conditions of stress was examd. by northern blotting anal., and the transcript level was increased under a cold-stressed (4.degree.) condition.
IT 307998-10-3
RL: PRP (Properties)
(amino acid sequence; cloning and expression of a gene encoding a putative chloroplast .omega.6 fatty acid desaturase of marine Chlamydomonas)

L11 ANSWER 23 OF 26 HCAPLUS COPYRIGHT 2008 ACS
ACCESSION NUMBER: 1998:[illegible] HCAPLUS
DOCUMENT NUMBER: 129:[illegible]
TITLE: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence. [Erratum to document cited in CA129:77224]
AUTHOR(S): Cole, S. T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S. V.; Eiglmeier, K.; Gas, S.; Barry, C. E., III; Tekaia, F.; Badcock, K.; Basham, D.; Brown, D.; Chillingworth, T.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Hornsby, T.; Jagels, K.; Krogh, A.; McLean, J.; Moule, S.; Murphy, L.; Oliver, K.; Osborne, J.; Quail, M. A.; Rajandream, M.-A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, J.; Squares, R.; Squares, S.; Sulston, J. E.; Taylor, K.; Whitehead, S.; Barrell, B. G.
CORPORATE SOURCE: Sanger Cent., Wellcome Trust Genome Campus, Hinxton, Cambs. CB10 1SA, UK
SOURCE: Nature (London, United Kingdom) (1998), 393(6685), 537-544
CODEN: NATUAS; ISSN: 0028-0836
PUBLISHER: Macmillan Magazines
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Table 1 was published with some symbols missing; the correct version can be found at http://www.sanger.ac.uk and is given here. In this, Rv1484 was incorrectly labeled as inhA instead of fabG1. Two of the genes in Mycobacterium tuberculosis were incorrectly identified: Rv1985c was not an [illegible] but an [illegible] gene, Rv1986 was not an [illegible] but an [illegible] gene, and Rv1987 was not an [illegible] but an [illegible]; Rv1988 is now designated thyX. The sequence of Rv1484 from M. bovis BCG-Pasteur

presented in Fig. 3 was interpreted as a single gene encoding a
putative integral membrane protein.

IT 208786-02-1
RL: PRP (Properties)
(deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence)

L11 ANSWER 24 OF 24 HCAPLUS COPYRIGHT 2006 ACS
ACCESSION NUMBER: 1998:61353 HCAPLUS
DOCUMENT NUMBER: 128:114937
TITLE: Cloning of a gene for chloroplast omega-3 desaturase from a green alga, Chlamydomonas reinhardtii
AUTHOR(S): Sato, Norihiro; Fujiwara, Shoko; Kawaguchi, Akihiko; Tsuzuki, Mikio
CORPORATE SOURCE: School of Life Science, Tokyo University of Pharmacy and Life Science, Tokyo, 192-03, Japan
SOURCE: Journal of Biochemistry (Tokyo) (1997), 122(6), 1234-1240
CODEN: JOBIAO; ISSN: 0021-924X
PUBLISHER: Japanese Biochemical Society

DOCUMENT TYPE: Journal
LANGUAGE: English

AB A gene for chloroplast .omega.6 desaturase, which catalyzes the desatn. of monoenoic to dienoic acids in chloroplasts, was isolated from Chlamydomonas reinhardtii. Because transformation was first performed with [illegible] .DELTA.12 desaturase of Synechocystis, using [illegible] DNA. An amplified DNA fragment of [illegible], encoding a transit for a protein homologous to these desaturases, was used as a probe for screening cDNA and genomic DNA libraries of C. reinhardtii. The cDNA clone of 2.2 kb obtained contained an open reading frame encoding a protein of 424 amino acids with a putative mol. mass of 48.4 kDa, the amino acid sequence of which showed 46-51% homol. to those of higher plant plastid .omega.6 and cyanobacterial .DELTA.12 desaturases. Introduction of the cloned genomic counterpart of this cDNA, designated as desC, into a Chlamydomonas mutant with defects in chloroplast .omega.6 desatn. and in the activities of photosystems I and II (PSI and PSII) complemented the desatn. mutation, indicating that the desC gene codes for chloroplast .omega.6 desaturase. The complemented strains did not recover from the photosynthetic lesions, but showed lower PSII activity at 45.degree. than the desatn. mutant, proving that the photosynthetic lesions in hf-9 are not caused by the desatn. mutation, and that the lowered unsatn. level of chloroplast lipids in the mutant is responsible for the expression of this high temp. of PSII activity, one of the thylakoid membrane functions.

IT **204279-00-5**
RL: BSU (Biological study, unclassified ; PRP (Properties); BIOL (Biological study)
(amino acid sequence; cloning and sequence of gene desC for chloroplast .omega.6 desaturase of a green alga, Chlamydomonas reinhardtii)

L11 ANSWER 26 OF 26 HCAPLUS COPYRIGHT 2013 ACS
ACCESSION NUMBER: 1996:936841 HCAPLUS
DOCUMENT NUMBER: 124:47157
TITLE: Identification and functional analysis of the transfer region of plasmid pMEA300 of the methylotrophic actinomycete Amycolatopsis methanolica
AUTHOR(S): Vrijbloed, J. W.; van der Put, N. M. J.; Dijkhuizen, L.
CORPORATE SOURCE: Dep. Microbiology, Univ. Groningen, Haren, 9751, Neth.
SOURCE: Journal of Bacteriology (1996), 177(22), 6499-505
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Amycolatopsis methanolica contains a 13.3-kb plasmid (pMEA300) that is present either as an integrated element or as an autonomously replicating plasmid. Conjugational transfer of pMEA300 results in pock formation, zones of growth inhibition that involve apoptosis, and high-frequency donor cell activity in a Streptomyces lividans 1326 genetic background. A 6.2-kb pMEA300 DNA segment specifying the functions of conjugation and pock formation was sequenced, revealing 10 open reading frames. This is the first sequence of the transfer region of a plasmid from a nonstreptomycete actinomycete. No clear similarities were found between the deduced sequences of the 10 putative Tra proteins of pMEA300 and those of Streptomyces plasmids. All Tra proteins of pMEA300 thus may represent unfamiliar types. A detailed mutational anal. showed that at least four Tra proteins, TraA (7,400 Da), TraH (6,700 Da), TraI (41,000 Da), and TraJ (31,000 Da), are required for efficient transfer of pMEA300. Their disruption resulted in a clear redn. in the conjugational transfer frequency, ranging from 10.2 times (TraJ) to 12.3 times (TraA), and in reduced pock sizes. At least two Tra proteins, TraA (7,400 Da) and TraB (31,000 Da), were shown to be

... [illegible] ... [illegible] ... [illegible] ...
... [illegible] ... [illegible] ... [illegible] ...
L1 171885-85-1
... [illegible] ... [illegible] ...
... [illegible] ... [illegible] ...
... [illegible] ... [illegible] ...

=> fil reg
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Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. See HELP
PROPERTIES for more information. See STNote 27, Searching Properties
in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

=>
=>

=>
=> d .seq l3 1-39

L3 ANSWER 1 OF 39 REGISTRY COPYRIGHT 2013 ACS
RN 487379-77-1 REGISTRY
CN GenBank BAA83822 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BAA83822 (Translated from: GenBank AB031546)
SQL 421

SEQ 1 MEKMKLVWGT TGLLKFELG TELKLMASVG HNAIWHFDLW KYTEKQRPRV
                                    ======

HITS AT: 230-237

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L3 ANSWER 2 OF 39 REGISTRY COPYRIGHT 2013 ACS
RN 487323-40-6 REGISTRY
CN GenBank BAB11133 (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank BAB11133 (Translated from: GenBank AB016844)
SQL 247

SEQ 1 MVILKFDLER IPENTVLLI TGANSGIGFA IAKVFMGNGA KVAIVDRNQE

HITS AT: [illegible]

RELATED SEQUENCES AVAILABLE WITH SEQLINK

L3 ANSWER 4 OF 39 REGISTRY COPYRIGHT 2013 ACS
RN 481335-47-1 REGISTRY
CN GenBank CAC42683 (9CI) (CA INDEX NAME
OTHER NAMES:
CN GenBank CAC42683 (Translated from: GenBank AY116491)
SQL 170

SEQ 51 KTLMELGNGP LRPWASIGHW LLWHFDLSKY RESEKPRVKI SLAAVFAFMA
                    = =====

HITS AT: 51-55

L3 ANSWER 5 OF 39 REGISTRY COPYRIGHT 2013 ACS
RN 481335-47-1 REGISTRY
CN GenBank CAC42683 (9CI) (CA INDEX NAME
OTHER NAMES:
CN GenBank CAC42683 (Translated from: GenBank AY116491)
SQL 170

SEQ 51 KTLMELGNGP LRPWASIGHW LLWHFDLSKY RESEKPRVKI SLAAVFAFMA
                    = =====

HITS AT: 51-55

L3 ANSWER 6 OF 39 REGISTRY COPYRIGHT 2013 ACS
RN 481335-47-1 REGISTRY
CN Protein (Human clone HFIEC13) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 104: PN: US20020165137 SEQID: 104 claimed protein
NTE

type	------ location ------	description
uncommon	Aaa-9[illegible]	-
uncommon	Aaa-[illegible]	-
uncommon	Aaa-[illegible]	-
uncommon	Aaa-141	-
uncommon	Aaa-14[illegible]	-

SQL 175

SEQ 51 AQRLRAGHEA EPSGWAAH PSSWEASA SVEYFPNYS VSPENASA

HITS AT: [illegible]

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: [illegible]

L3 ANSWER [illegible] OF 39 REGISTRY COPYRIGHT 2013 ACS

RN 487644-44-9 REGISTRY
CN Protein (Mycobacterium tuberculosis strain H37Rv gene MT0168) (9CI) (CA
    INDEX NAME)
OTHER NAMES:
CN GenBank AE000516-derived protein GI 15607870
SQL 276

SEQ 181 LQSRYTFFMA SLIFGILWGL WHFFLFVKD MYQYAFIHHE IWYAVMFFVG
                     === ===

HITS AT: 168-173

REFERENCE 1: 137:74267

L3 ANSWER 9 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 437141-30-5 REGISTRY
CN 6-Phosphogluconolactonase (Arabidopsis thaliana clone RAFL05-08-O12
    (RC98tt) gene At5g24400) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AF370305-derived protein GI 13878085
SQL 219

SEQ 51 GGSLIKSLRK LVESPYTDSI DWARWHFWV DERVIKNHD DSNYNLAYDS
                     ====

HITS AT: 72-77

REFERENCE 1: 137:

L3 ANSWER 10 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 437115-91-8 REGISTRY
CN Protein (human clone US20020048763-SEQID-44744 exon-encoded fragment)
    (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 4744: PN: US20020048763 SEQID: 44744 claimed protein
SQL 24

SEQ 1 NIIQLLEGFI HHGAWQMAWR AWHFKFILME SIEGLR
                    == ====

HITS AT: 19-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 137:

L3 ANSWER 11 OF 38 REGISTRY
RN [illegible] REGISTRY
CN L-Arginine, L-[(phosphinylmethyl)-L-leucyl]-L-leucyl-L-[(aminoiminomethyl)-L-
    lysyl]-L-alpha-glutamyl-L-tyrosyl-L-[(hydroxymethyl)-L-seryl]-L-histidyl-L-

histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-methionyl-L-.alpha.-glutamyl-L-seryl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:
CN 98: PN: WO0157275 SEQID: 34958 claimed protein
CN Protein (human clone WO0157275-SEQID-14[illegible]
SQL 36

SEQ 1 NIIQLLEGFI HHGAWQNAWR AWHFKFILME SIEGLR
== ====

HITS AT: 19-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:351357

L3 ANSWER 12 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 41[illegible]969-90-5 REGISTRY
CN L-Arginine, L-asparaginyl-L-isoleucyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-leucyl-L-.alpha.-glutamylglycyl-L-phenylalanyl-L-isoleucyl-L-histidyl-L-histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-methionyl-L-.alpha.-glutamyl-L-seryl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-leucyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 35[illegible]: PN: WO0157275 SEQID: 33858 claimed protein
CN Protein (human brain clone WO0157275-SEQID-33858 exon-encoded fragment)
SQL 36

SEQ 1 NIIQLLEGFI HHGAWQNAWR AWHFKFILME SIEGLR
== ====

HITS AT: 19-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:320295

L3 ANSWER 13 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 40[illegible]874-66-6 REGISTRY
CN Protein (Methanosarcina acetivorans strain C2A gene MA1162) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN GenBank AE010783-derived protein GI 19914997
SQL 289

SEQ 151 LQSRHTFFTA SIFFSILWSL WHFPLIFVNN MYQYEIFHEN VWIAVNFFVS
=== ===

HITS AT: 168-173

REFERENCE 1: [illegible]

L3 ANSWER 14 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 402671-83-4 REGISTRY
CN L-Arginine, L-asparaginyl-L-isoleucyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-leucyl-L-.alpha.-glutamylglycyl-L-phenylalanyl-L-isoleucyl-L-histidyl-L-histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-methionyl-L-.alpha.-glutamyl-L-seryl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-leucyl- (9CI) (CA INDEX NAME)

OTHER NAMES:
CN [illegible]
CN Protein (human bone marrow [illegible])
[illegible]
SQL [illegible]

SEQ 1 [illegible]
HITS AT: [illegible]

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: [illegible]

L3 ANSWER 15 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN [illegible] REGISTRY
CN Protein (human fetal liver clone [illegible]-SEQID-33514 exon-extended fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 528: PN: WO0157227 SEQID: 33514 claimed protein
SQL [illegible]

SEQ 1 [illegible]
HITS AT: 19-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: [illegible]

L3 ANSWER 16 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 400696-91-5 REGISTRY
CN Secretory protein (human clone HNNBM45 53-amino acid precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 96: PN: WO0216390 SEQID: 98 claimed protein
NTE

type	location		
unsure	Aaa-53	-	-

SQL 53

SEQ 1 [illegible]
HITS AT: 21-27

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: [illegible]

L3 ANSWER 17 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN [illegible] REGISTRY
CN L-Arginine, L-asparaginyl-L-isoleucyl-L-isoleucyl-L-glutaminyl-L-leucyl-L-leucyl-L-.alpha.-glutamylglycyl-L-phenylalanyl-L-isoleucyl-L-histidyl-L-histidylglycyl-L-alanyl-L-tryptophyl-L-glutaminyl-L-methionyl-L-alanyl-L-tryptophyl-L-arginyl-L-alanyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-lysyl-L-phenylalanyl-L-isoleucyl-L-leucyl-L-methionyl-L-.alpha.-glutamyl-L-seryl-L-isoleucyl-L-.alpha.-glutamylglycyl-L-[illegible] (9CI) (CA INDEX NAME)
OTHER NAMES:
CN [illegible]

CN   Protein (human placenta clone [illegible]-SEQ[illegible] exon-encoded fragment)
SQL 36

SEQ   1 MIIQLLFGFI HHGANQMANR ANHFKFILME SIEGLR
                                  == ====

HITS AT: [illegible]-24

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE   1: [illegible]

L3   ANSWER [illegible] OF 3[illegible] REGISTRY COPYRIGHT [illegible] ACS
RN   394342-[illegible]-2 REGISTRY
CN   SPERMIDINE SYNTHASE TRANSMEMBRANE PROTEIN (Ralstonia solanacearum strain GMI1000 gene speE1) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AL646[illegible]-derived protein GI 1[illegible]
SQL 5[illegible]

SEQ   151 VSLLFPLVLA PRLGLVRTGF LFGLGNTAIA VWTLWHFRAE LGLSARIRGA
                                                 ======

HITS AT: 182-187

REFERENCE   1: 136:145954

L3   ANSWER 19 OF 3[illegible] REGISTRY COPYRIGHT 2003 ACS
RN   394342-70-2 REGISTRY
CN   SPERMIDINE SYNTHASE PROTEIN (Ralstonia solanacearum strain GMI1000 gene speE2) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN   GenBank AL646084-derived protein GI 17431779
SQL 525

SEQ   151 LVSRVLTFDY LGALAVSLLF PLVLAPRLGL VRTGFLFGLG NTAIAVWTLW
                                                              ====
         201 HFRAELGLSA RIRGAMAMPA GMTAAALLAS FAASCRITHW SERALFGDEI
             ==

HITS AT: 197-202

REFERENCE   1: 136:145954

L3   ANSWER [illegible] OF 38 REGISTRY COPYRIGHT 2003 ACS
RN   354873-95-4 REGISTRY
CN   Musculoskeletal-associated antigen (human clone HFIEC13-883185 fragment) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN   1147: PN: WO0155367 SEQID: 1158 claimed protein
NTE

type	------ location ------			description
uncommon	Aaa-[illegible]	-	-	
uncommon	Aaa-9[illegible]	-	-	
uncommon	Aaa-1[illegible]	-	-	
uncommon	Aaa-141	-	-	
uncommon	Aaa-14[illegible]	-	-	

SQL 1[illegible]

SEQ   [illegible] [illegible]

HITS AT: [illegible]-71

RELATED SEQUENCES AVAILABLE WITH [illegible]

REFERENCE 1: [illegible]

L3 ANSWER 21 OF 38 REGISTRY COPYRIGHT 2013 ACS
RN [illegible]-3 REGISTRY
CN [illegible]
NTE

type	location	description
VARIANCE	Ala-Ile	- -

SQL 33

SEQ 1 MYELSHLFST KRLFLLALI WASVHFSYME ADAWTDESIP DRYLQAYLSI

HITS AT: 21-26

RELATED SEQUENCES AVAILABLE WITH [illegible]

REFERENCE 1: 135:535111

L3 ANSWER 22 OF 38 REGISTRY COPYRIGHT 2013 ACS
RN 354113-34-1 REGISTRY
CN L-Phenylalanine, L-methionyl-L-glutaminyl-L-leucyl-L-prolyl-L-isoleucyl-L-tryptophyl-L-leucyl-L-histidyl-L-leucyl-L-seryl-L-seryl-L-tyrosyl-L-isoleucyl-L-tryptophyl-L-leucyl-L-isoleucyl-L-tryptophyl-L-histidyl-L-phenylalanyl-L-arginyl-L-threonyl-L-methionyl-L-.alpha.-glutamyl-L-leucyl-L-isoleucyl-L-seryl-L-alanyl-L-seryl-L-valyl-L-leucyl-L-seryl-L-valyl-L-.alpha.-aspartyl-L-leucyl-L-leucyl-L-isoleucyl-L-leucylglycyl-L-leucyl-L-leucyl-L-tyrosyl-L-lysyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 176: PN: WO0157187 SEQID: 176 claimed protein
CN Bone marrow-specific protein (human clone WO0157187-SEQID-176 precursor)
SQL 43

SEQ 1 MQLPINLHLS SYIWLIWHFR TMELISASYL SYDLLILGLL YKF

HITS AT: 14-19

REFERENCE 1: 135:163431

L3 ANSWER 23 OF 38 REGISTRY COPYRIGHT 2013 ACS
RN [illegible]-3 REGISTRY
CN Bone marrow-specific protein (human clone WO0157187-SEQID-364 contig-encoded precursor) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 361: PN: WO0157187 SEQID: 364 claimed protein
NTE

type	location	description
VARIANCE	Ala-[illegible]	- -

SQL 96

SEQ 51 PWMQLPTWL HLSSYIWLIW HFRTMELISA SYLSYDLLIL GLLYKF

HITS AT: [illegible]

REFERENCE 1: [illegible]

L3 ANSWER 24 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN [illegible]-49-7 REGISTRY
CN Protein [illegible] (Physcomitrella patens clone [illegible] (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 24: PN: [illegible] SEQID: 174 claimed protein
MTE

type	------ location ------		description
[illegible]	[illegible]	-	-
[illegible]	[illegible]	-	-
[illegible]	[illegible]	-	-
[illegible]	[illegible]	-	-
[illegible]	[illegible]	-	-

SQL 178

SEQ 51 AQRLRAGHRA GGTGCWGAWH FSGSWRGSLA SVGPVPPNVS VSQPFXFXSA
==== =

HITS AT: 66-71

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 135:163414

L3 ANSWER 25 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 343286-49-7 REGISTRY
CN Protein LMRP (Physcomitrella patens clone 55_ck5_b04fwd lipid metabolism-related) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 241: PN: [illegible] SEQID: [illegible]
SQL 178

SEQ 51 PATKTLMELG MGPLRPWASI GHWLLWHFDL SKYRESEKPR VKISLAAVPA
==== ====

HITS AT: 73-78

REFERENCE 1: 135:19831

L3 ANSWER 26 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 307998-10-3 REGISTRY
CN Desaturase, fatty acid .omega.6-(Chlamydomonas strain W-80) (9CI) (CA INDEX NAME)
SQL 421

SEQ 201 QEKMKDWNGV TSALFKFFLG TFLKLWASVG HWAIWHFDLN KYTEKQRPRV
==== =

HITS AT: 231-237

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:2473

L3 ANSWER 27 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN [illegible]-46-5 REGISTRY
CN Protein, Arabidopsis thaliana clone [illegible] (9CI) (CA INDEX NAME
OTHER NAMES:
CN 969: PN: [illegible] SEQID: [illegible] claimed protein
SQL 206

SEQ 51 PAPLIKQLRV IMSPTVLIL IWAPWHFFWI LFTYIENHP FSNYKLAYIS
==== =

HITS AT: 71-77

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 133:318297

L3 ANSWER 28 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 302645-68-4 REGISTRY
CN Protein (Arabidopsis thaliana clone [illegible]) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 968: PN: EP1033405 SEQID: 60968 claimed protein
SQL 325

SEQ 101 ADLSDKFCKE RGAFTVVVSG GSLIKSLRKL VESPYVDSID WARWHFFWVD
======

HITS AT: 141-146

REFERENCE 1: 133:318297

L3 ANSWER 29 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 302411-43-4 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2113368) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 163: PN: EP1033405 SEQID: 55163 claimed protein
SQL 256

SEQ 51 GGSLIKSLRK LVESPYVDSI DWARWHFFWV DERVVPKNHD DSNYKLAYDS
======

HITS AT: 72-77

REFERENCE 1: 133:318296

L3 ANSWER 30 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 302411-42-3 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_2113367) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 162: PN: EP1033405 SEQID: 55162 claimed protein
SQL 325

SEQ 101 ADLSDKFCKE RGAFTVVVSG GSLIKSLRKL VESPYVDSID WARWHFFWVD
======

HITS AT: 141-146

REFERENCE 1: 133:318296

L3 ANSWER 31 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 301564-27-2 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_1025180) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1596: PN: EP1033405 SEQID: 7409 claimed protein
SQL 256

SEQ 51 GGSLIKSLRK LVESPYVDSI DWARWHFFWV DERVVPKNHD DSNYKLAYDS
======

HITS AT: 72-77

REFERENCE 1: 133:306360

L3 ANSWER 32 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 301564-26-1 REGISTRY
CN Protein (Arabidopsis thaliana clone Ceres_1025179) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1595: PN: EP1033405 SEQID: 7408 claimed protein
SQL 325

SEQ 101 [illegible] WARWHFFWTL
=====

HITS AT: 141-146

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 133:30656[illegible]

L3 ANSWER 33 OF 38 REGISTRY COPYRIGHT [illegible] ACS
RN [illegible]6839-2[illegible]-4 REGISTRY
CN L-Phenylalanine, L-tryptophyl-L-valyl-L-alanyl-L-tryptophyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 13: PN: W[illegible]44771 SEQID: [illegible] unclaimed sequence
SQL 6

SEQ 1 WVAWHF
======

HITS AT: 1-6

REFERENCE 1: 133:145916

L3 ANSWER 34 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 286839-22-3 REGISTRY
CN L-Phenylalanine, L-tryptophyl-L-alanyl-L-arginyl-L-tryptophyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 12: PN: WO0044771 SEQID: 21 unclaimed sequence
SQL 6

SEQ 1 WARWHF
======

HITS AT: 1-6

REFERENCE 1: 133:145916

L3 ANSWER 35 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 286839-16-5 REGISTRY
CN L-Phenylalanine, L-tryptophyl-L-valyl-L-arginyl-L-tryptophyl-L-histidyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 2: PN: WO0044771 SEQID: 2 claimed sequence
SQL 6

SEQ 1 WVRWHF
== ===

HITS AT: 1-6

REFERENCE 1: 133:145916

L3 ANSWER 36 OF 38 REGISTRY COPYRIGHT 2003 ACS
RN 2[illegible]86-[illegible]-1 REGISTRY
CN Protein [illegible] Mycobacterium [illegible] (CA INDEX NAME)
OTHER NAMES:
CN GenBank AL[illegible]-derived protein GI [illegible]
SQL 230

SEQ 1 MITRYKFFSS [illegible] KRPHTKIIWH PTHADNLP[illegible] ITAGPLLATS

HITS AT: [illegible]

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: [illegible]

REFERENCE [illegible]

L3 ANSWER 37 OF 38 REGISTRY COPYRIGHT [illegible]
RN 214273-11-[illegible] REGISTRY
CN Desaturase, fatty acid .omega.6- (Chlamydomonas reinhardtii clone pCD1 gene desF reduced) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN .omega.6 Desaturase (Chlamydomonas reinhardtii clone pCD1 gene desF reduced)
[illegible]
SQL 424

SEQ 201 VTEADMAKWD STSAMLYKVF LGTPLKLWAS VGHWLVWHFD LNKYTPKQRT

HITS AT: 234-239

REFERENCE 1: [illegible]

L3 ANSWER 38 OF 38 REGISTRY COPYRIGHT [illegible]
RN 171885-85-1 REGISTRY
CN Protein TraH (plasmid pMEA300) (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Protein TraH (Amycolatopsis methanolica plasmid pMEA300)
SQL 116

SEQ 1 MFTPEPKPTT DHTGQSTTEA VEARRAADLA IYTNAKYPTR TTQTVSWIGW

51 HFGELSGNVV PLGLGAAVWD GFYALSLLTA LGMAANELRL RRQQRAVRTR
==
HITS AT: 47-52

REFERENCE 1: [illegible]

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FILE COVERS 1907 - 13 Feb 2003  VOL 138: ISS 7
FILE LAST UPDATED: 11 Feb 2003  (20030211/ED)

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

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=> d stat que l15
L1             1 SEA FILE=REGISTRY ABB=ON  PLU=ON  WVRWHF/SQSP
L2          1110 SEA FILE=REGISTRY ABB=ON  PLU=ON  W[GAILVSTKRHF][GAILVSTKRHF]W[
                 GAILVSTKRHF]F/SQSP
L3            38 SEA FILE=REGISTRY ABB=ON  PLU=ON  W[GAILVSTR][GAILVSTR]WHF/SQSP

L5             1 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L1
L6           [illegible] SEA FILE=HCAPLUS ABB=ON  PLU=ON  L2
L7             1 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L3 AND L6
L12            [illegible] SEA FILE=REGISTRY ABB=ON  PLU=ON  L4 AND SQL=<60
L13           [illegible] SEA FILE=HCAPLUS ABB=ON  PLU=ON  L12
L14           [illegible] SEA FILE=HCAPLUS ABB=ON  PLU=ON  L13 NOT (2003 OR 2002)/PY
L15           [illegible] SEA FILE=HCAPLUS ABB=ON  PLU=ON  L14 NOT (L6 OR L7)

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=>
=>

=> d ibib abs hitrn l15 1-17

L15  ANSWER 1 OF 17  HCAPLUS  COPYRIGHT 2003 ACS
ACCESSION NUMBER:         2002:36295  HCAPLUS
DOCUMENT NUMBER:          136:151515
TITLE:                    Peptide [illegible] and their [illegible] hybridization in
                          human tissues
INVENTOR(S):              Tang, Y. Tom; Lin, Shaofeng; Dimitrov, Radoje T.
PATENT ASSIGNEE(S):       Hyseq, Inc., USA
SOURCE:                   PCT Int. Appl., 147 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
LANGUAGE:                 English
FAMILY ACC. NUM. COUNT:   1
PATENT INFORMATION:

     PATENT NO.         KIND  DATE          APPLICATION NO.  DATE
```

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001092523	A2	20011206	WO 2001-XA10836	20010529
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001092523	A3	20011206	WO 2001-IB01836	20010529
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.:

US 2000-577409	A	20000518

AB The present invention provides a collection or library of 13,901 nucleic acid contig sequences assembled from expressed sequence tag or cDNA libraries isolated mainly by sequencing by hybridization (SBH), std. PCR, Sanger sequencing techniques, and in some cases, sequences obtained from one or more public databases. The cDNA libraries are from human tissue sources and nearest neighbor sequence homologies are provided. The invention also relates to the proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins. [This abstr. record is the fourth of four records for this document necessitated by the large no. of index entries required to fully index the document and publication system constraints.].

IT **432700-32-8**
RL: ANT (Analyte); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); USES (Uses)
(amino acid sequence; nucleic acids and their encoded polypeptides from human tissues)

L15 ANSWER 2 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:895070 HCAPLUS
DOCUMENT NUMBER: 137:16519
TITLE: Human polypeptide fragments and their encoding cDNA polynucleotides
INVENTOR(S): Shimkets, Richard A.; Leach, Martin D.
PATENT ASSIGNEE(S): Curagen Corporation, USA
SOURCE: PCT Int. Appl., 1037 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 5
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001092523	A2	20011206	WO 2001-XA10836	20010529
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
WO 2001092523	A3	20011206	WO 2001-IB01836	20010529
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				

DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: US 2001-[illegible]P 20010[illegible]
US 2001-[illegible]P 20010[illegible]
US 2001-[illegible]P 20010[illegible]
US 2001-[illegible]P 20010[illegible]
US 2001-[illegible]P 20010[illegible]

AB The present invention provides 11,491 ORFX, novel human polypeptide fragments, as well as the 11,491 cDNA fragments encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivs., variants, mutants, or fragments of the ORFX polypeptides, polynucleotides, or antibodies. The invention addnl. provides methods in which the ORFX polypeptides, polynucleotides, and antibodies are used in diagnostic and treatment of a broad range of pathol. states, as well as other uses. [This abstr. record is one of thousands that could not be displayed by the large no. of index entries required to fully link them to current publication system constraints.].

IT **434378-63-9P**
RL: ANT (Analyte); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; human polypeptide fragments and their encoding cDNA polynucleotides)

L15 ANSWER 3 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:273192 HCAPLUS
DOCUMENT NUMBER: 133:295042
TITLE: Selection of an immunogenic and protective epitope of the PsaA protein of Streptococcus pneumoniae using a phage display library
AUTHOR(S): Srivastava, N.; Zeiler, J. L.; Smithson, S. L.; Carlone, G. M.; Ades, E. W.; Sampson, J. S.; Johnson, S. E.; Kieber-Emmons, T.; Westerink, M. A. J.
CORPORATE SOURCE: Department of Medicine, Medical College of Ohio, Toledo, OH, 43614, USA
SOURCE: Hybridoma (2000), 19(1), 23-31
CODEN: HYBRDY; ISSN: 0272-457X
PUBLISHER: Mary Ann Liebert, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Streptococcus pneumoniae is a leading cause of bacterial meningitis in young and elderly individuals. The currently available polysaccharide vaccines have limited efficacy in those age groups most susceptible to pneumococcal infections. This study focuses on mapping the epitopes of a surface protein of S. pneumoniae by biopanning a 15 mer phage display library using 3 different monoclonal antibodies (MAbs) against the Pneumoccal surface adhesin A (PsaA). PsaA is a component of the bacterial cell wall that is highly species specific and is involved in bacterial adherence and virulence. Biopanning of the phage display library reveals three distinct epitopes on the PsaA protein. The sequence homol. of these epitopes ranges from two to six amino acids when compared to the native PsaA protein type 2. Two of these epitopes have been evaluated for their immunogenicity in mice. The peptide selected by the MAbs 8G12, 6F6, and 1B7 is referred to as the consensus peptide and is immunogenic in mice. Optimal anti-PsaA response is obsd. in mice immunized with 5 [illegible] of the consensus peptide complexed to proteosomes in 1:1 ratio. The anti-PsaA response is significantly [illegible] than the [illegible] protein. The peptide selected by the MAb 1B7 is the [illegible] form is similarly [illegible] serotype 2 when [illegible] mice immunized with the native protein. These results show that the selected epitopes of PsaA protein are immunogenic and protective in mice. These epitopes need to be evaluated further as alternatives to currently available vaccines.

IT **301300-56-1**

BL: BAC Biological activity or effects, except adverse ; BPN Biological study, unclassified ; THU Therapeutic use ; BIOL Biological study ; USES (Uses)
Psaa protein of Streptococcus pneumoniae in vaccine against streptococcal infections

REFERENCE COUNT: [illegible]

L15 ANSWER 4 OF 17 HCAPLUS COPYRIGHT [illegible]
ACCESSION NUMBER: [illegible]
DOCUMENT NUMBER: 131:19[illegible]
TITLE: Epitope peptides immunogenic against Streptococcus pneumoniae and their use in vaccines
INVENTOR(S): Carlone, George M.; Ades, Edwin W.; Sampson, Jacquelyn S.; Tharpe, Jean A.; Zeller, Joan Louise; Westerink, Maria Anna Julia
PATENT ASSIGNEE(S): The Government of the United States of America, Represented by the Secretary, USA
SOURCE: PCT Int. Appl., 59 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9945121	A1	19990910	WO 1999-US4326	19990226
W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2326408	AA	19990910	CA 1999-2326408	19990226
AU 9927950	A1	19990920	AU 1999-27950	19990226
BR 9908476	A	20001205	BR 1999-8476	19990226
EP 1060249	A1	20001220	EP 1999-908543	19990226
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: [illegible] US 1998-[illegible]P P 19980302
WO 1999-US4326 W 19990226

AB Peptides are provided which immunospecifically bind to monoclonal antibodies specific for the 37-kDa pneumococcal surface adhesion A protein (PsaA) of Streptococcus pneumoniae of the invention, and that are immunogenic against Streptococcus pneumoniae infection. Also provided are vaccines comprising such immunogenic polypeptides, and methods of conferring protective immunity against Streptococcus pneumoniae infection by administering therapeutic compns. comprising the immunogenic peptides of the invention. Also provided are methods of detecting the presence of Streptococcus pneumoniae in a sample using antibodies or antigens, and methods of preventing and treating Streptococcus pneumoniae infection in a subject. In addn. a phage display method of identifying the sequence of a peptide potentially capable of eliciting protective immunity against a pathogenic microorganism is provided.

IT **241814-51-7P**
BL: BAC Biological activity or effects ; PAC Properties ; THU Therapeutic use ; BIOL Biological study ; PREP Preparation ; USES (Uses)
(epitope peptides immunogenic against Streptococcus pneumoniae and their use in vaccines

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2011 ACS
ACCESSION NUMBER: 1998:415241 HCAPLUS
DOCUMENT NUMBER: 129:76489
TITLE: Heparin- and sulfatide-binding peptides from the type I repeats of human thrombospondin and conjugates thereof for treatment of metastatic tumors and other neovascularization-related diseases
INVENTOR(S): Roberts, David D.; Browning, Phillip J.; Bryant, Joseph L.; Lawler, John W.; Krutzsch, Henry C.; Ye, Nanghua
PATENT ASSIGNEE(S): United States Dept. of Health and Human Services, USA
SOURCE: U.S., 133 pp., Cont.-in-part of U. S. 215,088, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 5770563	A	19980623	US 1995-487568	19950607
US 801812	A0	19921215	US 1991-801812	19911206
US 5357041	A	19941018		
US 6051549	A	20000418	US 1998-41119	19980311

PRIORITY APPLN. INFO.: US 1991-801812 A2 19911206
US 1994-215085 B2 19940321
US 1995-487568 A1 19950607

OTHER SOURCE(S): MARPAT 129:76489

AB This invention identifies a biol. active group of peptide sequences from Type I repeat units of the extracellular matrix protein, human thrombospondin-1, identical or homologous to the sequence, KRFKQDGGWSHWSPWSSC (SEQ ID NO:30). The biol. activities residing with the full sequences, portions thereof, and variants of the full or partial sequences are disclosed. The [illegible] may be enhanced by covalently linking these peptides to [illegible], preferably a branched, water-sol. polymer of low or absent toxicity and immunogenicity, such as polysucrose (Ficoll). The invention describes (1) a method for prepg. such conjugates, (2) the use of the defined peptides or their conjugates in blocking or modifying the action on cellular processes of heparin (e.g., proliferation, adhesion, motility, extravasation and neovascularization), sulfatides, related sulfated glycoconjugates, fibronectin, and basic fibroblast growth factor, involving malignant cell lines and normal endothelial cells. Use of the defined peptides, analogs or peptidomimetics and their conjugates for treatment of metastatic tumors, breast carcinomas, melanomas, Kaposi's sarcomas, hemangiomas, diabetic retinopathies, and various pathol. conditions dependent upon neovascularization is also disclosed.

IT 209457-55-6
RL: BAC (Biological activity or effector, except adverse); BFR (Biological process); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)
(heparin- and sulfatide-binding peptides from the type I repeats of human thrombospondin and conjugates thereof for treatment of metastatic tumors and other neovascularization-related diseases)

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L16 ANSWER 1 OF 1 HCAPLUS COPYRIGHT 2011 ACS
ACCESSION NUMBER: 1998:415241 HCAPLUS
DOCUMENT NUMBER: 129:76489

TITLE: A region from the medium chain adaptor subunit (.mu.) recognizes leucine- and tyrosine-based sorting signals
AUTHOR(S): Ohno, Hiroshi; Fournier, Marie-Claude; Poy, Gisele; Bonifacino, Juan S.
CORPORATE SOURCE: Cell Biology and Metabolism Branch, National Institute of Child Health and Human Development, National Institutes of Health, Bethesda, MD, 20892-2425, USA
SOURCE: Journal of Biological Chemistry (1998), 273(41), 26937-26943
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Tyrosine-based sorting signals in the cytosolic tails of membrane proteins have been found to bind directly to the medium chain subunit (.mu.) of the adaptor complexes AP-1 and AP-2. For the leucine-based signals, an interaction with AP-1 and AP-2 has been reported, but no specific interacting subunit has been demonstrated. After searching for mols. interacting with the leucine-based sorting signals within the cytosolic tail of the major histocompatibility complex class II-assocd. invariant chain using a phage display approach, we identified phage clones with homol. to a conserved region of the AP-1 and AP-2 .mu. chains. To investigate the relevance of these findings, we have expressed regions of mouse .mu.1 and .mu.2 chains on phage gene product III and investigated the binding to tail sequences from various transmembrane proteins with known endosomal targeting signals. Enzyme-linked immunosorbent binding assays showed that these phages specifically recognized peptides contg. functional leucine- and tyrosine-based sorting signals, suggesting that these regions of the .mu.1 and .mu.2 chains interact with both types of sorting signals.

IT **208192-30-7P**
RL: BPN (Biosynthetic preparation); BIM (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PREP (Preparation); PROC (Process)
(region from medium chain adaptor subunit (.mu.) of AP-1 and AP-2 recognizes leucine- and tyrosine-based sorting signals)

REFERENCE COUNT: 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L15 ANSWER 7 OF 17 HCAPLUS COPYRIGHT 2013 ACS
ACCESSION NUMBER: 1998:11596 HCAPLUS
DOCUMENT NUMBER: 128:110913
TITLE: Amino acids within residues 181-200 of the nicotinic acetylcholine receptor .alpha.1 subunit involved in nicotine binding
AUTHOR(S): Lentz, Thomas L.; Chaturvedi, Vijaya; Conti-Fine, Bianca M.
CORPORATE SOURCE: Department of Cell Biology, Yale University School of Medicine, New Haven, CT, [illegible]
SOURCE: Biochemical Pharmacology (1998), [illegible], 441-447
CODEN: BCPCA6; ISSN: 0006-2952
PUBLISHER: Elsevier Science Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Structural determinants of L-[3H]nicotine binding to the sequence flanking Cys 192 and Cys 193 of the Torpedo acetylcholine receptor .alpha.1 subunit were investigated using synthetic peptides, residues 181-[illegible], and fusion proteins, residues 181-[illegible]. Nicotine binding at a single conc. (50 nM) was compared with 13 peptides and fusion proteins in which individual amino acids of peptide 181-200 were substituted. Substitution of Lys 187, Tyr 190, Cys 192, Cys 193, Thr 196, and Tyr 198 resulted in the greatest redn. in nicotine binding. Equil. binding of [3H]nicotine to peptide 181-200 revealed a binding component with an apparent Kd of 1.2

.Ka.M. substitution. Lys 1[illegible], Asn 1[illegible], Tyr 1[illegible], Tyr 1[illegible], Tyr 193, and Tyr 198 resulted in a significant redn. in affinity. Affinity was not affected significantly by substitution of Arg 1[illegible], Lys 145 (with Gly or Arg), Val 1[illegible], Tyr 153, Pro 1[illegible], Asp 1[illegible], Thr 196, and Asp 201. It is concluded that Lys 1[illegible], His 1[illegible], Tyr 19[illegible], Lys 19[illegible], Cys 1[illegible], and Tyr 1[illegible] play the greatest role in nicotine binding to residues 181-[illegible] of the .alpha.1 subunit. Tyrosines have implicated Tyr 1[illegible], Lys 1[illegible], Tyr 1[illegible], and Tyr 1[illegible] in agonist binding to the acetylcholine receptor. These results confirm a role for these residues and also demonstrate a function for Lys 1[illegible] and His 1[illegible] in nicotine binding.

IT **201529-09-1**
RL: BPR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(181-201 nicotinic receptor .alpha.1-subunit mutant; nicotinic acetylcholine receptor .alpha.1 subunit residues 181-2[illegible] in nicotine binding)

L15 ANSWER 9 OF 1[illegible] HCAPLUS COPYRIGHT [illegible] ACS
ACCESSION NUMBER: 1[illegible]:[illegible] HCAPLUS
DOCUMENT NUMBER: 1[illegible]:11[illegible]
TITLE: Isolation and characterization of antibodies which specifically recognize the peptide encoded by exon 7 (v2) of the human CD44 gene
AUTHOR(S): Borgya, A; Woodman, A; Sugiyama, M; Donie, F; Kopetzki, E.; Matsumura, Y; Tarin, D
CORPORATE SOURCE: Boehringer Mannheim GmbH, Penzberg, D-[illegible], Germany
SOURCE: Clinical Molecular Pathology (1995), 48(5), M241-M250
CODEN: CMPAFI; ISSN: 1355-2910
PUBLISHER: BMJ Publishing Group
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Exon 7 of the human CD44 gene is overexpressed in many commonly occurring carcinomas. The aim of the study was to explore the diagnostic and therapeutic potential of this frequent abnormality. A new monoclonal antibody (mAb, M-23.6.1) and a polyclonal antibody (pAb, S-[illegible]) to the corresponding antigen were raised by immunizing mice and sheep, resp., with a specially constructed fusion protein HIV2 (gp32)-CD44 exon 7. Characterization of mAb M-23.6.1 by ELISA, Western blotting, immunocytochem., and FACS anal. confirmed that it specifically recognizes an epitope in the region between amino acids 19 and 33 of the peptide encoded by this exon. Western blotting expts. with two cell lines, BT[illegible] and ZR75-1, known from RT-PCR data to be over-transcribing the exon, yielded a monospecific band of approx. [illegible] kDa, and immunocytochem. showed discrete membrane staining on the same cell lines. Fluorescent antibody cell sorting (FACS) revealed binding to greater than 90% of the cells of each of these lines. Specificity of recognition of the antigen was shown by inhibition of the precise immunoreactivity typically seen in ELISA and Western blots, by pre-incubation with synthetic exon 7 peptide or fragments of it. The new antibodies will be useful tools for the further anal. of abnormal CD44 isoforms and their clin. implications.
IT **172997-35-2**
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(isolation and characterization of monoclonal antibody to peptide encoded by exon 7 of human CD44)

L15 ANSWER 9 OF 1[illegible] HCAPLUS COPYRIGHT [illegible] ACS
ACCESSION NUMBER: 1[illegible]:[illegible] HCAPLUS
DOCUMENT NUMBER: 1[illegible]:[illegible]
TITLE: [illegible]
AUTHOR(S): [illegible]

AU Fuchs, Sara
CORPORATE SOURCE: Dep. Chemical Immunology, Weizmann Inst. Science, Rehovot, 76100, Israel
SOURCE: Proceedings of the National Academy of Sciences of the United States of America, 1990, 87(18), 7148-52
CODEN: PNASA6; ISSN: 0027-8424
PUBLISHER: Natl Acad Sciences
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The ligand binding site of the nicotinic acetylcholine receptor is localized in the .alpha.-subunit within a region that includes cysteine and tyr. By analyzing the ligand binding in animal species that are resistant to .alpha.-neurotoxins, the authors have previously shown that for residues in this region, at positions 187, 189, 194, and 197, differ between animals sensitive (e.g., mouse) and resistant (e.g., mongoose and snake) to .alpha.-bungarotoxin (.alpha.-BTX). In the present study, the authors performed site-directed mutagenesis on a fragment of the mongoose AcChoR .alpha.-subunit (residues 122-205) and exchanged residues 187, 189, 194, and 197, either alone or in combination, with those present in the mouse .alpha.-subunit sequence. Only the mongoose fragment in which all four residues were mutated to the mouse ones exhibited .alpha.-BTX binding similar to that of the mouse fragment. The mongoose double mutation in which Leu-194 and His-197 were replaced with proline residues, which are present at these positions in the mouse AcChoR and in all other toxin binders, bound .alpha.-BTX to .apprxeq.60% of the level of binding exhibited by the mouse fragment. In addn., replacement of either Pro-194 or -197 in the mouse fragment with serine and histidine, resp., markedly decreased .alpha.-BTX binding. All other mutations resulted in not to just a small increase in .alpha.-BTX binding. These results have led the authors' to propose two subsites in the binding domain for .alpha.-BTX: the proline subsite, which includes Pro-194 and -197 and is crit. for .alpha.-BTX binding, and the arom. subsite, which includes amino acid residues 187 and 189 and dets. the extent of .alpha.-BTX binding.

IT **170662-94-9**, EARGWKHWVFYACCLTTHYLD **170662-98-3**, EARGWKHWVFYACCPTTHYLD **170662-99-4**, EARGWKHWVFYACCLTTPYLD **170663-00-0**, EARGWKHWVFYACCPTTPYLD
RL: BFR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(mongoose nicotinic receptor .alpha.-subunit binding domain mutant contg.; nicotinic receptor .alpha.-subunit .alpha.-bungarotoxin-binding domain arom. subsite and proline subsite)

IT **170663-01-1**, EARGWKHWVFYSCCPTTPYLD
RL: BFR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(mouse nicotinic receptor .alpha.-subunit binding domain contg.; nicotinic receptor .alpha.-subunit .alpha.-bungarotoxin-binding domain arom. subsite and proline subsite)

IT **170663-02-2**, EARGWKHWVFYSCWPTTPYLD **170663-03-3**, EARGWKHWVFYSCCSTTPYLD **170663-04-4**, EARGWKHWVFYSCCPTTHYLD
RL: BFR (Biological process); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PROC (Process)
(mouse nicotinic receptor .alpha.-subunit binding domain mutant contg.; nicotinic receptor .alpha.-subunit .alpha.-bungarotoxin-binding domain arom. subsite and proline subsite)

L16 ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2013 ACS
ACCESSION NUMBER: 1990:[illegible] HCAPLUS
DOCUMENT NUMBER: 113:[illegible]
TITLE: Profile of the regions of acetylcholine receptor .alpha. chain recognized by T-lymphocytes and by antibodies in EAMG-susceptible and non-susceptible mice after different peripheral immunization

[illegible] with the record:
AUTHOR(S): Oshima, Mikani; Barthel, Andrew B.; Atassi, M. Zouhair
CORPORATE SOURCE: Dep. Biochem., Baylor Coll. Med., Houston, TX, 77030, USA
SOURCE: Molecular Immunology (1994), 31(11), 833-41
CODEN: MOIMD5; ISSN: 0161-5890
DOCUMENT TYPE: Journal
LANGUAGE: English
AB SJL/J (B6) mice develop a neuromuscular disease, exptl. autoimmune myasthenia gravis (EAMG), after .gtoreq.2 immunizations with Torpedo californica acetylcholine receptor (AChR). To det. whether EAMG is related to recognition of particular region(s) on the main extracellular domain of the .alpha. chain (residues .alpha. 1-210) in prolonged immunization, the authors have exam. the differences in the antibody and T cell recognition profiles of B6 and SJL (a strain that does not develop EAMG) mice after different periods and a no. of immunization with Torpedo AChR. In a given strain, antibodies and T cells recognized immunodominant regions, which may coincide or may be uniquely B cell or T cell determinants. Both B6 and SJL exhibited similar antibody recognition profiles after the 2nd and through the 4th immunizations with AChR. Major differences between the 2 strains were in and in their T cell recognition of regions in the second part (residues 101-210) of the main extracellular domain of the .alpha. chain. T cells of SJL recognized predominantly only one region (111-126) within this part of the .alpha. chain, whereas in B6, T cell recognition of 3 peptides (111-126, 146-162, and 182-198) and next neighbor regions to them persisted throughout the period. Of these 3 peptides, 146-162 was an immunodominant peptide unique to B6, as the other 2 peptides (111-126 and 182-198) were also recognized by either T cells or antibodies in SJL. To study the role of T cells recognizing region 146-162 in EAMG, a T cell line was generated against this region and the cells transferred into B6 mice followed by one Torpedo AChR injection. Enhancement of antibody prodn. toward .alpha. chain peptides was obsd. as an influence of T cell transfer compared to profiles at 1 wk. In addn., 1 out of 3 mice exam. showed signs of EAMG. These results suggest the importance of T cells recognizing residues 146-162 in EAMG. Thus, the presence of persistent T cell responses to the second half (residues 100-210) of the main extracellular domain of the .alpha. chain is assocd. with the development of EAMG in B6 mice, while absence of these responses in SJL mice may enable them to escape the disease. The presence of the immunodominance of peptide 146-162 in [illegible] probably most important for the pathogenesis [illegible]
IT **157960-63-9**
RL: BIOL (Biological study)
(in B- and T-cell epitope mapping on acetylcholine receptor .alpha. chain, autoimmune myasthenia gravis in relation to)

L15 ANSWER 11 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1994:318925 HCAPLUS
DOCUMENT NUMBER: 121:318925
TITLE: Diagnosis of tumors by assay of CD44 splicing patterns
INVENTOR(S): Tarin, David; Matsumura, Yasuhiro
PATENT ASSIGNEE(S): ISIS Innovation Ltd., UK
SOURCE: PCT Int. Appl., 41 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9412643	A1	1994[illegible]	WO 1993-GB2[illegible]	1993[illegible]
W: JP, US				

DESIGNATED STATES: W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM

EP 611824 A1 19940817 EP 1993-916130 19930721

EP 611824 B1 19980617

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE

JP [illegible] A [illegible] JP 1993-514271 19930721

AT [illegible] E [illegible] AT 1993-916130 19930721

ES [illegible] A1 [illegible] ES 1993-916130 19930721

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE

GR [illegible] A [illegible] GR 1993-401[illegible] 19930[illegible]

EP [illegible] A1 [illegible] EP 1994-[illegible] 19940[illegible]

R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LI, LU, MC, NL, PT, SE

US 5531646 A 19960702 US 1995-473[illegible] 19950607

US 5770693 A 19980623 US 1996-[illegible] 19960[illegible]

PRIORITY APPLN. INFO.:

GB 1992-15[illegible] 19920721

GB 1991-24[illegible] 19911122

GB 1992-26[illegible] 19921214

WO 1993-GB1520 19930720

WO 1993-GB2394 19931122

AB There is marked over-expression of multiple spliced variants of the CD44 gene in tumor compared to counterpart normal tissue. This observation forms the basis of a method of diagnosing neoplasia by anal. of a sample of body tissue or body fluid or waste product. A new exon 6, of 129 bp, has been found and sequenced, and is claimed as such and for use in the diagnostic method. Samples of breast tumors were assayed for CD44 mRNA by reverse transcription/PCR using primers to detect hematopoietic CD44 followed by hybridization with a probe from exon 4. A no. of splice variants were found in neoplastic tissue that were absent from normal tissue, this was found in all patients tested. There was a difference in splice patterns between neoplastic and non-neoplastic diseased tissues (cystic disease). Similar results were found in colon cancer using biopsy and stool samples and in bladder cancer using urine samples for diagnosis.

IT **155216-25-4**

RL: PRP (Properties)
(amino acid sequence of, in neoplastic tissue, altered splicing patterns in neoplastic tissue in relation to)

L15 ANSWER 12 OF 17 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 1992:564026 HCAPLUS

DOCUMENT NUMBER: 117:164026

TITLE: Species- and subtype-specific recognition by antibody WF6 of a sequence segment forming an .alpha.-bungarotoxin binding site on the nicotinic acetylcholine receptor .alpha. subunit

AUTHOR(S): McLane, K. E.; Fritzen, M.; Wu, X.; Diethelm, B.; Maelicke, A.; Conti-Tronconi, B. M.

CORPORATE SOURCE: Coll. Biol. Sci., Univ. Minnesota, St. Paul, MN, 55108, USA

SOURCE: Journal of Receptor Research (1992), 12(3), 199-211
CODEN: JRREDC; ISSN: 0197-1115

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The monoclonal antibody WF6 competes with acetylcholine and .alpha.-bungarotoxin (.alpha.-BGT) for binding to the Torpedo nicotinic acetylcholine receptor (nAChR) .alpha.1 subunit. By using synthetic peptides corresponding to the complete Torpedo nAChR .alpha.1 subunit, the authors previously mapped a continuous epitope recognized by WF6, and the prototope for .alpha.-BGT, to the sequence segment .alpha.1(181-200). Single amino acid substitution analogs have been used as an initial approach to det. the str. anal. basis for WF6 and .alpha.-BGT binding. In the present study, the authors determine the anal. of the structural features of the WF6 epitope by comparing its cross-reactivity with

synthetic peptides corresponding to the alpha.1 subunit of the muscle nAChRs of different species, the rat brain .alpha.2, .alpha.3, .alpha.4 and .alpha.5 nAChR subtypes, and the Torpedo .alpha.-like protein subunits, .alpha.P1TEI .alpha.1, and .alpha.P2TEI .alpha.2. The results indicate that MF6 is able to cross-react with the muscle .alpha.1 subunits of different species by virtue of conservation of several critical amino acid residues between positions 191-195 of the .alpha.1 subunit. These studies further define the essential structural features of the sequence segment .alpha.1 (181-210) required to form the epitope for MF6.

IT **133295-54-2 133322-53-9**
RL: BIOL (Biological study)
(antibody; nicotinic receptor .alpha.-bungarotoxin binding site binding by, structure in relation to)

L16 ANSWER 13 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1991:223857 HCAPLUS
DOCUMENT NUMBER: 114:223857
TITLE: Structural determinants of .alpha.-bungarotoxin binding to the sequence segment 181-200 of the muscle nicotinic acetylcholine receptor .alpha. subunit: species-specific amino acid substitutions
AUTHOR(S): McLane, Kathryn E.; Wu, Xiadong; Diethelm, Brenda; Conti-Tronconi, Bianca M.
CORPORATE SOURCE: Coll. Biol. Sci., Univ. Minnesota, St. Paul, MN, 55108, USA
SOURCE: Biochemistry (1991), 30(20), 4925-34
CODEN: BICHAW; ISSN: 0006-2960
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The sequence segment 181-200 of the Torpedo nicotinic acetylcholine receptor (nAChR) .alpha. subunit forms a binding site for .alpha.-bungarotoxin (.alpha.-BTX). Synthesis peptides corresponding to the homologous sequences of human, calf, mouse, chicken, frog, and cobra muscle nAChR .alpha.1 subunits were tested for their ability to bind 125I-.alpha.-BTX, and differences in .alpha.-BTX affinity were detd. by using soln. (IC50) and a solid-phase (Kd) assays. Panels of overlapping peptides corresponding to the complete .alpha.1 subunit of mouse and human were also tested for .alpha.-BTX binding, but other sequence segments forming the .alpha.-BTX site were not consistently detectable. The Torpedo .alpha.1(181-200) and the homologous frog and chicken peptides bound .alpha.-BTX with higher affinity (Kd .apprx. 1-2 .mu.M, IC50 .apprx. 1-2 .mu.M) than the human and calf peptides (Kd .apprx. 5-6 .mu.M, IC50 .apprx. 15 .mu.M). The mouse peptide bound .alpha.-BTX weakly when attached to a solid support (Kd .apprx. 8 .mu.M) but was effective in competing for 125I-.alpha.-BTX in soln. (IC50 .apprx. 1 .mu.M). The cobra nAChR .alpha.1-subunit peptide did not detectably bind .alpha.-BTX in either assay. Amino acid substitutions were correlated with .alpha.-BTX binding activity of peptides from different species. The role of a putative vicinal disulfide bond between cysteine-192 and -193, relative to the Torpedo sequence, was detd. by modifying the peptides with sulfhydryl reagents. Reln. and alkylation of the peptides decreased .alpha.-BTX binding, whereas oxidn. of the peptides had little effect. Modifications of the cysteine cystine residues of the cobra peptide failed to induce .alpha.-BTX binding activity. Thus, while the adjacent cysteines are likely to be involved in forming the main .alpha.1-subunit interface a vicinal disulfide bound was not required for .alpha.-BTX binding.

IT **133295-54-2P 133322-53-9P**
RL: SPN (Synthetic preparation); PREP (Preparation)
(prepn. and .alpha.-bungarotoxin binding by, main binding site of nicotinic acetylcholine receptor .alpha. subunit in relation to

IT **133295-53-1P**
RL: SPN (Synthetic preparation); PREP (Preparation)

[illegible]

L15 ANSWER 14 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1991:525236 HCAPLUS
DOCUMENT NUMBER: 115:125236
TITLE: [illegible]
AUTHOR(S): [illegible]
CORPORATE SOURCE: [illegible]
SOURCE: [illegible]
DOCUMENT TYPE: [illegible]
LANGUAGE: [illegible]
AB .alpha.-Cobratoxin and acetylcholine receptor .alpha.-subunit complementary binding domain peptide (residues 173-181) were studied by 1-D and 2-D NMR spectroscopy. A model for binding is proposed.
IT 114753-46-7
RL: BIOL (Biological study)
(.alpha.-cobratoxin binding by, conformation in, NMR study of)

L15 ANSWER 15 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1988:516189 HCAPLUS
DOCUMENT NUMBER: 109:116189
TITLE: Binding of .alpha.-bungarotoxin to synthetic peptides corresponding to residues 173-204 of the .alpha. subunit of Torpedo, calf, and human acetylcholine receptor and restoration of high-affinity binding by sodium dodecyl sulfate
AUTHOR(S): Wilson, Paul T.; Lentz, Thomas L.
CORPORATE SOURCE: Sch. Med., Yale Univ., New Haven, CT, [illegible], USA
SOURCE: Biochemistry [illegible], [illegible], [illegible]
CODEN: BICHAW; ISSN: [illegible]
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To investigate structure-function relations of a segment of the acetylcholine receptor .alpha. subunit, binding of .alpha.-bungarotoxin to synthetic peptides corresponding to residues 173-204 of Torpedo, calf, and human .alpha. subunits was compared using a solid-phase radioassay. The affinities of ^{125}I-labeled .alpha.-bungarotoxin for the calf and human peptides were 15- and 150-fold less, resp., than for the Torpedo peptide. On the basis of nonconservative substitutions in the calf and human sequences, arom. residues (Tyr-181, Trp-187, and Tyr-189) are important for the higher affinity binding of the Torpedo peptide. Substitution of neg. charged Glu-180 with uncharged Gln in the calf peptide did not significantly affect toxin binding, indicating Glu-180 alone does not comprise the anionic subsite on the receptor to which the cationic quaternary ammonium groups of cholinergic agents bind. d-Tubocurarine competed with toxin binding to the modified calf [illegible] with [illegible] Glu-181 and Asp-196 present in Torpedo. Thus, the [illegible] subsite could be formed by another neg. charged residue or by >1 amino acid side chain. It is possible that the pos. charges on cholinergic ligands are countered by a neg. electrostatic potential provided by polar groups, such as the hydroxyl group of tyrosine, present in several residues in this region, and the neg. charges present on any of residues 175, 176, 177, [illegible]. Equil. satn. binding of .alpha.-bungarotoxin to Torpedo peptide 173-204 revealed a major binding component with an apparent K_d of [illegible] nM and a major component with a K_d of [illegible] nM. In the presence of 0.1% SDS, a binding component with a K_d of [illegible] nM was detected. This compares with an affinity of K_D = 0.41 nM for toxin binding to native acetylcholine receptor in the solid-phase assay. SDS may stabilize a conformation of the peptide that is conducive to high-affinity binding.

IT **115826-29-4 115826-30-7**
RL: PYP (Physical process); RCT (Reactant); RACT (Reactant or reagent)
[illegible]

L15 ANSWER 16 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1988:4[illegible] HCAPLUS
DOCUMENT NUMBER: 109:1[illegible]
TITLE: .alpha.-Toxin binding to acetylcholine receptor .alpha.179-191 peptides: intrinsic fluorescence studies
AUTHOR(S): Radding, W.; Canfield, R. W. R.; Levinson, L. S.; Hashim, S. A.; Low, P. W.
CORPORATE SOURCE: Howard Hughes Inst., Columbia Univ., New York, NY, 10032, USA
SOURCE: FEBS Letters (1988), 231(1), 212-16
CODEN: FEBLAL; ISSN: 0014-5793
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Interactions between 2 .alpha.-toxins and the synthetic peptides .alpha.179-191 from both calf and human acetylcholine receptor .alpha.-subunit sequences were studied by measurements of quenching of intrinsic fluorescence after toxin addn. Dissocn. consts. of .apprx.5 .times. 10-8M for binding of calf peptide by both .alpha.-cobrotoxin and erabutoxin a were estd. The binding of .alpha.-cobrotoxin to calf peptide, which leads to marked quenching of fluorescence intensity, is inhibited by a 1[illegible]M excess of acetylcholine. The human .alpha.179-191 peptide binds to .alpha.-cobrotoxin, but not, under comparable conditions, to erabutoxin a.
IT **114753-46-7P**
RL: SPN (Synthetic preparation); PREP (Preparation)
(prepn. of, of calf acetylcholine receptor .alpha.-subunits, and .alpha.-toxins binding by)

L15 ANSWER 17 OF 17 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1984:185956 HCAPLUS
DOCUMENT NUMBER: 100:185956
TITLE: A super active cyclic hexapeptide analog of somatostatin
AUTHOR(S): Veber, Daniel F.; Saperstein, Richard; Nutt, Ruth F.; Freidinger, Roger M.; Brady, Stephen F.; Curley, Paul; Perlow, Debra S.; Paleveda, William J.; Colton, C. Dylion; et al.
CORPORATE SOURCE: Merck Sharp and Dohme Res. Lab., West Point, PA, 19486, USA
SOURCE: Life Sciences (1984), 34(14), 1371-8
CODEN: LIFSAK; ISSN: 0024-3205
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Cyclo(N-methyl-Ala-Tyr-D-Trp-Lys-Val-Phe) (I) [81377-02-8] was 50-100-fold more potent than cyclic somatostatin [38916-34-6] for the inhibition of insulin [9004-10-8], glucagon [9007-92-5] and growth hormone [9002-72-6] release as revealed by structure-activity studies of cyclic hexapeptide analogs of somatostatin in rats. The hydroxyl group of tyrosine conferred a 10-fold enhancement to the potency. Potency was also correlated with hydrophobicity. I improved the control of postprandial hyperglycemia in diabetic animals when given in combination with insulin. The analog was quite stable in the blood and in the gastrointestinal tract, but the bioavailability after oral administration was only 1-3%. The biol. properties and long duration of I should allow clin. evaluation of the inhibition of glucagon release as an adjunct to insulin in the treatment of patients with diabetes.
IT **89808-58-2**
RL: PYP (Physical process); RCT (Reactant); RACT (Reactant or reagent)

somatotropin secretion inhibition by, structure in relation to,

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E4 THROUGH E28 ASSIGNED

=> fil reg
FILE 'REGISTRY' ENTERED AT 13:54:27 ON 13 FEB 2003
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
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STRUCTURE FILE UPDATES:    12 FEB 2003  HIGHEST RN 489395-83-1
DICTIONARY FILE UPDATES:  12 FEB 2003  HIGHEST RN 489395-83-1

TSCA INFORMATION NOW CURRENT THROUGH MAY 20, 2002

  Please note that search-term pricing does apply when
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Crossover limits have been increased.  See HELP CROSSOVER for details.

Experimental and calculated property data are now available.  See HELP
PROPERTIES for more information.  See STNote 27, Searching Properties
in the CAS Registry File, for complete details:
http://www.cas.org/ONLINE/STN/STNOTES/stnotes27.pdf

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=> s e4-e28 and l12
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1 301300-56-1/BI
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1 432700-32-8/BI
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(434378-63-9/RN)
1 89808-58-2/BI
(89808-58-2/RN)

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L16 ANSWER 1 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN **434378-63-9** REGISTRY
CN L-Isoleucine, L-methionyl-L-seryl-L-tryptophyl-L-histidyl-L-seryl-L-tryptophyl-L-isoleucyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-.alpha.-glutamyl-L-isoleucyl-L-tyrosyl-L-leucyl-L-.alpha.-glutamyl-L-asparaginyl-L-threonyl-L-prolyl-L-cysteinyl-L-tyrosyl-L-lysyl-L-tyrosyl-L-.alpha.-glutamyl-L-threonyl-L-.alpha.-aspartyl-L-isoleucyl-L-leucyl-L-tyrosyl-L-isoleucyl-L-alanyl-L-seryl-L-phenylalanyl-L-.alpha.-aspartyl-L-phenylalanyl-L-seryl-L-arginyl-L-glutaminyl-L-isoleucyl-L-prolyl-L-seryl-L-threonyl-L-methionyl-L-arginyl-L-isoleucyl-L-seryl-L-valyl-L-tyrosyl-L-seryl-L-valyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 3444: PN: WO0190523 SEQID: 8440 claimed protein
CN Protein (human clone WO0190523-SEQID-8440 fragment)
SQL **50**
RN **434378-63-9** REGISTRY
SQL **50**

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HITS AT: 3-8

REFERENCE 1: 137:16518

L16 ANSWER 2 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN **432700-32-8** REGISTRY
CN L-Threonine, L-glutaminyl-L-asparaginyl-L-leucyl-L-threonyl-L-alanyl-L-glutaminyl-L-.alpha.-aspartylglycyl-L-valyl-L-glutaminyl-L-tryptophyl-L-cysteinyl-L-.alpha.-aspartyl-L-leucylglycyl-L-seryl-L-leucyl-L-glutaminyl-L-prolyl-L-prolyl-L-leucyl-L-prolyl-L-seryl-L-seryl-L-tryptophyl-L-.alpha.-aspartyl-L-tyrosyl-L-arginyl-L-arginyl-L-.alpha.-glutamyl-L-seryl-L-leucyl-

L-[illegible]-L-prolyl-L-[illegible]-L-[illegible]-L-phenylalanyl-L-phenylalanyl-L-
[illegible]-L-phenylalanyl-L-tryptophyl-L-lysyl-L-arginyl-L-tryptophylglycyl-
L-phenylalanyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN [illegible]: PN: WO0164835 SEQID: 26885 claimed protein
CN Protein (human clone WO0164835-SEQID-26885 fragment)
SQL **47**
RN **432700-32-8** REGISTRY
SQL **47**

SEQ 1 [illegible]

HITS AT: 41-46

REFERENCE 1: [illegible]

L16 ANSWER 3 OF 25 REGISTRY COPYRIGHT [illegible] ACS
RN **301300-56-1** REGISTRY
CN L-Tyrosine, N-(1-oxohexadecyl)-L-threonyl-L-valyl-L-arginyl-L-seryl-L-
valyl-L-prolyl-L-tryptophyl-L-threonyl-L-alanyl-L-tryptophyl-L-alanyl-L-
phenylalanyl-L-histidylglycyl- (9CI) (CA INDEX NAME)
NTE modified

type	------ location ------		description
modification	Thr-1	-	1-oxohexadecyl<Pal>

SQL **15**
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SQL **15**

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====== ==

HITS AT: 7-12

REFERENCE 1: [illegible]

L16 ANSWER 4 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN **241814-51-7** REGISTRY
CN L-Tyrosine, L-threonyl-L-valyl-L-seryl-L-arginyl-L-valyl-L-prolyl-L-
tryptophyl-L-threonyl-L-alanyl-L-tryptophyl-L-alanyl-L-phenylalanyl-L-
histidylglycyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 1: PN: WO0204497 SEQID: 5 claimed protein
SQL **15**
RN **241814-51-7** REGISTRY
SQL **15**

SEQ 1 TVSRVPWTAW AFHGY
====== ==

HITS AT: 7-12

REFERENCE 1: [illegible]

REFERENCE 2: 136:117869

REFERENCE 3: [illegible]

L16 ANSWER 5 OF 25 REGISTRY COPYRIGHT [illegible] ACS
RN **209457-55-6** REGISTRY
CN L-Serine, L-lysyl-L-[illegible]-L-phenylalanyl-L-lysyl-L-[illegible]-L-[illegible]-
[illegible]-L-tryptophyl-L-[illegible]-L-tryptophyl-L-seryl-
L-phenylalanyl-L-tryptophyl-L-seryl- (9CI) (CA INDEX NAME)

SQL 15
RN 172997-35-2 REGISTRY
SQL 15

SEQ 1 TKCNFRNSLEI ESHSW

HITS AT: 4-9

REFERENCE 1: 128:11091З

L16 ANSWER 8 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 172997-35-2 REGISTRY
CN L-Lysinamide, L-threonyl-L-tryptophyl-L-.alpha.-aspartyl-L-tyrosyl-L-

SEQ 1 TRGWNHWYET TCCEDTEYLD

HITS AT: 4-9

REFERENCE 1: 128:110913

L16 ANSWER 7 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 201529-09-1 REGISTRY
CN L-Aspartic acid, L-tyrosyl-L-arginyl-L-tryptophyl-L-lysyl-L-histidyl-

SQL 20
RN 201529-09-1 REGISTRY
SQL 20

SEQ 1 TRGWNHWYET TCCEDTEYLD

HITS AT: 4-9

REFERENCE 1: 129:91865

L16 ANSWER 6 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 208192-30-7 REGISTRY
CN Glycine, L-alanyl-L-.alpha.-aspartyl-L-alanyl-L-tyrosyl-L-

SQL 18
RN 208192-30-7 REGISTRY
SQL 18

SEQ 1 KEELLFMC MLFMCI

HITS AT: 4-14

REFERENCE 1: 129:71494

L16 ANSWER 5 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 209457-55-6 REGISTRY
CN L-Lysinamide, L-threonyl-L-tryptophyl-L-.alpha.-aspartyl-L-tyrosyl-L-

L16 ANSWER 10 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170663-04-4 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-histidyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170663-04-4 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YSCCSTTPYL D
==========
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 11 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170663-03-3 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-tryptophyl-L-prolyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170663-03-3 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YSCWSTTPYL D
==========
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 12 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170663-02-2 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-tryptophyl-L-prolyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170663-02-2 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YSCWFTTPYL D
==========
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 13 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170663-01-1 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170663-01-1 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YSCCSTTPYL D
==========
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 13 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170663-00-0 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-cysteinyl-L-leucyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170663-00-0 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YACTPTTPYL P
======
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 14 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170662-99-4 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-cysteinyl-L-leucyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170662-99-4 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YACPTTPYL P
======
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 15 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170662-98-3 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-histidyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170662-98-3 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YACPTTHYL P
======
HITS AT: 5-10

REFERENCE 1: 123:330219

L16 ANSWER 16 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 170662-94-9 REGISTRY
CN L-Aspartic acid, L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-histidyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
SQL 21
RN 170662-94-9 REGISTRY
SQL 21

SEQ 1 EARGWKHWVF YACPTTHYL P
======
HITS AT: 5-10

REFERENCE 1: [illegible]

L16 ANSWER 17 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 157960-63-9 REGISTRY
CN L-Tyrosine, L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-glutamyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 17
RN 157960-63-9 REGISTRY
SQL 17

SEQ 1 RGWKHWFYSC CPTTTY
HITS AT: 3-8

REFERENCE 1: [illegible]

L16 ANSWER 18 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 155216-25-4 REGISTRY
CN L-Alanine, L-threonyl-L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-leucyl-L-histidyl-L-threonyl-L-threonyl-L-threonyl-L-glutaminyl-L-methionyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Antigen CD 44 (human exon 6)
SQL 43
RN 155216-25-4 REGISTRY
SQL 43

SEQ 1 TLMSTSATAT ETATKRQETW DWFSWLFLPS ESKNHLHTTT QMA
HITS AT: 22-27

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: [illegible]

L16 ANSWER 19 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 133322-53-9 REGISTRY
CN L-Aspartic acid, L-alanyl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-seryl-L-cysteinyl-L-cysteinyl-L-prolyl-L-threonyl-L-threonyl-L-prolyl-L-tyrosyl-L-leucyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN 20
RN 133322-53-9 REGISTRY
SQL 20

SEQ 1 ARGWKHWIFY SCCPTTPYLD
HITS AT: 4-9

REFERENCE 1: [illegible]

REFERENCE 2: [illegible]

L16 ANSWER 20 OF 25 REGISTRY COPYRIGHT 2003 ACS
RN 133295-54-2 REGISTRY
CN L-Aspartic acid, L-seryl-L-tryptophylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-cysteinyl-L-

[illegible]ystathionyl-L-pr[illegible]lyl-L-seryl-L-thr[illegible]tyl-L-pr[illegible]lyl-L-tyr[illegible]syl-L-l-valyl- 9:1
(CA INDEX NAME)

SQL 20
RN   133295-54-2 REGISTRY
SQL 20

SEQ   1 [illegible]

HITS AT: 4-9

REFERENCE   1: 117:164916

REFERENCE   2: 114:223467

L16 ANSWER 21 OF 25 REGISTRY COPYRIGHT [illegible] ACS
RN   133295-53-1 REGISTRY
CN   L-Serine, L-.alpha.-glutamyl-L-seryl-glycyl-L-.alpha.-glutamyl-L-tryptophyl-
     L-valyl-L-isoleucyl-L-lysyl-L-.alpha.-glutamyl-L-alanyl-L-arginylglycyl-L-
     tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-
     tyrosyl- (9CI) (CA INDEX NAME)
SQL 20
RN   133295-53-1 REGISTRY
SQL 20

SEQ   1 SGEWVMKESR GWKHWVFYTC CPSTPYLDIT YH
                   ======
HITS AT: 12-17

REFERENCE   1: 114:223467

L16 ANSWER 22 OF 25 REGISTRY COPYRIGHT 2013 ACS
RN   115826-30-7 REGISTRY
CN   L-Histidine, L-seryl-glycyl-L-.alpha.-glutamyl-L-tryptophyl-L-valyl-L-
     methionyl-L-lysyl-L-.alpha.-glutamyl-L-seryl-L-arginylglycyl-L-tryptophyl-
     L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-
     threonyl-L-cysteinyl-L-cysteinyl-L-prolyl-L-seryl-L-threonyl-L-prolyl-L-
     tyrosyl-L-leucyl-L-.alpha.-aspartyl-L-isoleucyl-L-threonyl-L-tyrosyl-
     (9CI) (CA INDEX NAME)
SQL 32
RN   115826-30-7 REGISTRY
SQL 32

SEQ   1 SGEWVMKESR GWKHWVFYTC CPSTPYLDIT YH
                   ======
HITS AT: 12-17

REFERENCE   1: 114:223467

L16 ANSWER 23 OF 25 REGISTRY COPYRIGHT [illegible] ACS
RN   115826-29-4 REGISTRY
CN   L-Histidine, L-seryl-glycyl-L-.alpha.-glutamyl-L-tryptophyl-L-valyl-L-
     isoleucyl-L-lysyl-L-glutamyl-L-seryl-L-arginylglycyl-L-tryptophyl-L-
     lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl-L-alanyl-L-
     cysteinyl-L-cysteinyl-L-prolyl-L-seryl-L-threonyl-L-prolyl-L-tyrosyl-L-
     leucyl-L-.alpha.-aspartyl-L-isoleucyl-L-threonyl-L-tyrosyl- (9CI) (CA
     INDEX NAME)
SQL 32
RN   115826-29-4 REGISTRY
SQL 32

SEQ   1 SGEWVKQEN GNKHWVFYAC CPSTPYLDIT YH
                   ======
HITS AT: 12-17

REFERENCE 1: [illegible]

L16 ANSWER 24 OF 25 REGISTRY COPYRIGHT [illegible] ACS
RN 114753-46-7 REGISTRY
CN L-Alanine, L-lysyl-L-.alpha.-glutamyl-L-seryl-L-arginylglycyl-L-tryptophyl-L-lysyl-L-histidyl-L-tryptophyl-L-valyl-L-phenylalanyl-L-tyrosyl- (9CI) (CA INDEX NAME)
SQL 13
RN 114753-46-7 REGISTRY
SQL 13

SEQ 1 KESRGWKHWV FYA
[illegible]
HITS AT: 6-11

REFERENCE 1: 113:128235

REFERENCE 2: 113:[illegible]

L16 ANSWER 25 OF 25 REGISTRY COPYRIGHT [illegible] ACS
RN 89808-58-2 REGISTRY
CN Cyclo(N-methyl-L-alanyl-2-iodo-L-phenylalanyl-D-tryptophyl-L-lysyl-L-valyl-L-tryptophyl) (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN 1,4,7,10,13,16-Hexaazacyclooctadecane, cyclic peptide deriv.
CN Cyclic(N-methyl-L-alanyl-2-iodo-L-phenylalanyl-D-tryptophyl-L-lysyl-L-valyl-L-tryptophyl)
MTE cyclic
modified

type	location	description
modification	Ala-1 -	methyl<Me>
modification	Phe-2 -	iodo<I>

SQL 6
RN 89808-58-2 REGISTRY
SQL 6

SEQ 1 AFWKVW
======
HITS AT: 1-2, 3-6

REFERENCE 1: [illegible]